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                                                                                                                                                                         ; MOLECULE TYPE: DNA
US-08-400-256-34
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RESULT 6
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                                                                                                                             Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ACYLATED INSULIN NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Andersen, Asse: APPLICANT: Markussen, Jan
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                                            230 CGACAAAACGGTAAAA 245
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                                                                             18 CGACAAAACGGTAAAA 33
                                                                                                            Local Similarity hes 16; Conserv
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nes 16; Conserv
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STRANDEDNESS: single
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405 Lexington Avenue, 64th Floor
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Andersen, Asser Sloth
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100.0%; Pred. No.
                                                                                                                         100.0%;
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US-08-975-365-19

; Sequence 19, Application US/08975365

; Patent No. 6011007
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; MOLECULE TYPE:
US-08-400-256-43
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                               APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
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APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLAN
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: No. 60110
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                                                                                                                                                                            TITLE OF INVENTION: ACYLATED INSULIN NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 CGACAAAACGGTAAAA 245
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REFERENCE/DOCKET NUMBER: 3985.220-US
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CITY: New York
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CITY: New York
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TELEFAX: 212-878-9655
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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8-08-975-365-6-4
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8-980-357-30
98-980-357-70-3
98-285-819A-16
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40, Appl
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50	Query Ma Best Loc Matches	ATTORNEY AGAIN INFORMATION: NAME: Jane Massey Licata REGISTRATION NUMBER: 32,257 REFERENCE/DOCKET NUMBER: TJU-13 TELECOMMUNICATION INFORMATION: TELEFAN: (609) 779-2400 TELEFAX: (609) 779-8488 INFORMATION FOR SEO ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 61 TYPE: Nucleic Acid STRANDEDNESS: Single TUPOTOGY: Linear NATI-SENSE: NO	COMED	COMPU	ULT 1 08-563- equence atent N SENERAL APPLI TITLE	44	2 8 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	22222222 8000122450
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GAATTCAG	llarity Conser	INT INF INT	JEST TEN 4 SYSTEM SYSTEM WORDP JICATION NUMB TE: NO ATION: NICHON NUMB NUMB NUMB NUMB NUMB NUMB NUMB NUM	COURNCE ADD COURT TO Lakerry Hi grry Hi grry Hi J USA USA VDABLE) pplicat 2095 AATION: Kmiec /ENTION	19.7	1111111	21.22
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	Gaps					25, App	25, Appl 3, Appl 13, Appl 3, Appl 13, App 13, App	149, Appli 3, Appli 6, Appli 1, Appli 1, Appli 4, Appli 4, Appli 1, Appli 1, Appli
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US-08-400 256-40
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                                                                                                                                                                                                                    : Sequence 40, Application US/08975365
: Patent No. 6011007
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Patent No. 5750497
                                                                                                                                                                                                                                                                                                                                                                                                       Mat ches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                   CORRESPONDENCE ADDRESS
                                                                                                    APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
                                                                                                                                                             APPLICANT: Havelund, APPLICANT: Halstrom,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
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                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                      PUTLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                227 CGACAAAACGGTAAAA 242
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CITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lambiris, Elias J. REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America
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               STREET:
                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                    18 CGACAAAACGGTAAAA 33
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New York
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               405 Lexington Avenue, 64th Floor
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                                 No. 6011007o No. 6011007disk of No. 6011007th America, Inc
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                                                                                      ACYLATED INSULIN
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                               ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen
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ATTORNEY/AGENT INFORMATION:
                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                           CURRENT APPLICATION DATA:
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ADDRESSE: No. 57504970 No. 5750497disk of No. 5750497th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
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MEDIUM TYPE: Floppy disk
                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ACYLATED INSULIN
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                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTMAKE: Patentin Bolosom ""
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STRANDEDNESS: single
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REGISTRATION NUMBER: 33
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                                        REFERENCE/DOCKET NUMBER:
                                                                            NAME
                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                    CITY: New York
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TELEPHONE:
                                                         NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33
                                                                                                                                       FILING DATE:
                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                              Patentin Release #1.0, Version #1.25
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                                                                                                                      03-MAR-1995
N: 514
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                                                                                                                                                          US/08/400,256
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ER: 3985.220-US
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Best Local Similarity 100.08; Pred. No. 6.4;
Matches 16; Conservative 0; Mismarkhom
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                                                                      Matches
                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/400,256
FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
AITORNEY/ACENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-867-0123
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPEKATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: ACYLATED INSULIN
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230 CGACAAAACGGTAAAA 245
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CITY: New York
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STRANDEDNESS: single
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                                  18 CGACAAAACGGTAAAA 33
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                                                                  16: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                            linear
                                                                                    24.2%; Score 16; DB 1; 100.0%; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19:
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                                                                  Mismatches
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                                                                                                   Length 523;
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                                                                  Indels
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RESULT 6

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MESOL/1 7
US-08-975-365-19
Sequence 19, Application US/08975365
Patent No. 6011007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 24.2%; Score 16; DH 1; Length 523; Best Local Similarity 100.0%; Pred. No. 6.4; Matches 16; Conservative 0; Mismatches 0; Indels
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APPLICANT: Havelu
APPLICANT: Halstr
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                                                                                                                                                                                                                                                 APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, 1b
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM_PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6011007o No. 6011007disk of No. 6011007th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.
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APPLICANT: Markussen, Jan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                       TITLE OF INVENTION: ACYLATED INSULIN NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FITLE OF INVENTION: ACYLATED INSULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 CGACAAAACGGTAAAA 245
                                            COUNTRY: United States of America 21P: 10174-6401
                                                                                        STREET: 405 Le:
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 CGACAAAACGGTAAAA 33
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TELEFAX: 212-878-9655
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REFERENCE/DOCKET NUMBER: 3985.220-US
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CLASSIFICATION: 514
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H: 523 base pairs
nucleic acid
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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APPLICANT: Markussen, Jan
TITLE OF INVESTION: ACYLATED INSULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 523 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                        FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                      COMPUTER: IBM PC comparince
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 CGACAAAACGGTAAAA 245
                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                        REFERENCE/DOCKET NUMBER:
                                                                                           NAME
                                                                                                                                                                                  CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                   REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POPOLOGY:
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                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                       Lambiris, Elias J
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                                                                                                                                                                                                                                                                                                                                                                                New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          523 base pairs
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                                                                                                                                                                                                                                                                                       FE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 6011007o No. 6011007disk of No. 6011007th America, Inc
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                                                                                                                                               US 08/400,256
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                                                      3985.220-US
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                                                                                           Best
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                                                                       Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 523 base pairs
                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Havelund,
APPLICANT: Halstrom,
APPLICANT: Jonassen,
                                                                                                                                                              MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Markussen, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA
230 CGACAAAACGGTAAAA 245
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                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                    18 CGACAAAACGGTAAAA 33
                                                                                                                                                                                  : ASOTOdol.
                                                                                                                                                                                               LENGTH: 523 base pair
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 3985.220-US
                                                                                                                                                                                                                                                                                                                                                            NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/400,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/975, 365
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                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                       16:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6011007
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                                                                                                                                                                                                                                523 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 Lexington Avenue, 64th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                                                                                                        212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersen, Asser Sloth
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Havelund, Svend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 6011007o No. 6011007disk of No. 6011007th America, Inc
                                                                                                                                                                                                                                                                                                          212-867-0123
                                                                                       100.08;
                                                                                       24.2%; Score 16; DB 3; Length 524; 100.0%; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.2%; Score 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34:
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                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 524;
                                                                       Indels
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                                                                                                                                                                                                                                                                                                                     US-08-975-365-46
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                                                                                                                                                                                                                                                                             Sequence 46, Application US/08975365 Patent No. 5011007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 46, Application US/08400256 Patent No. 5750497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 391
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
AUTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderser
APPLICANT: Markusse
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Havelund, APPLICANT: Halstrom,
                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                              APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
                                                                                                                                                                                                                       APPLICANT: Havelund, Sveno
APPLICANT: Halstrom, John
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                                                                                                                                                                                                                                                                                                                                                                                              227 CGACAAAACGGTAAAA 242
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CITY: New York
                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 535 base pairs
ZIP: 10174-6401
                    COUNTRY: United States of America
                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                    New York
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                                                                        405 Lexington Avenue, 64th Floor
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                                                                                                                                                                                                                                             Havelund, Svend
                                                                                          No. 6011007o No. 6011007disk of No. 6011007th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.2%; Score 16; DB 1 100.0%; Pred. No. 6.4;
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                                                                                                                                  49
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TOPOLOGY: linear; MOLECULE TYPE: DNAUS-08-975-365-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 49, Application US/08400256
Patent No. 5750497
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 46:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 535 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                   REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                   NAME: Lambiris, Elias J.
                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ACYLATED INSULIN NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 CGACAAAACGGTAAAA 242
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                                                                                                                                                                                                                                                                                                                                                                                          STREET: 405 Le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 3985.220-US
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                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 03-MA
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: 212-878-9655
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                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                              REGISTRATION NUMBER:
                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.
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                                                                                                                 Lambiris, Elias J
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                     212-878-9655
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N: 514
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 Mismatches

                                                                             3985.220-US
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                                                              Matches
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                                                                          Best Local Similarity
                                                                                          Query Match
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                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 538 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: No. 6011007o No. 6011007disk of No. 6011007th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ACYLATED INSULIN
227 CGACAAAAGGGTAAAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 CCACAAAACGGTAAAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
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Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                              18 CGACAAAACGGTAAAA 33
                                                                                                                                                         STRANDEDNESS: single
ToPoLoGY: linear
                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
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                                                                                                                                                                                           TYPE:
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                                                                                                                                                                                                                                                                                                                                    NAME
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/400,256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                      538 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Markussen, Jan
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                                                                                                                                                                                                                                                                     212-867-0123
                                                                         24.2%: Score 16;
100.0%; Pred. No.
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    Mismatches

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                                                             Mismatches
                                                                                        DB 3; Length 538;
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Ouery Match

Best Local Similarity

Matches 15; Conservat
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US-08-136-993-15/c
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 7, Application US/08735545
; Patent No. 6025131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-136-993-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Takaqi, Siroshi APPLICANT: Aratuka, Shino APPLICANT: Matsui, Siroshi APPLICANT: Matsui, Siroshi APPLICANT: Mashizu, Kinya APPLICANT: Kotkeda, Satoshi APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC:DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear nucleic acid (synthetic DNA)
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                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Van Dyk, Tina K. APPLICANT: LaRossa, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 5.0 SEQ
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CITY: N.W.
STATE: Was
   STREET: AVE.
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STATE:
                                                                                                ADDRESSEE:
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                                                                                                                                    ADDRESSEE: E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 TGAGATCTGGATCCG 2
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DELAWARE
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                                                            E: E. I. DU PONT DE NEMGURS
E: AND COMPANY
1007 MARKET STREET
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                                                                                                                                                                                                                                                                                                                                         Robert Alan
                                                                                                                                                                                                                                                                 Identifying Regulated
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COMPUTER READABLE FORM:

19898

UNITED STATES OF AMERICA

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US-08-735-545-7
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: Patent No. 6194159
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                                                            ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA A.
REGISTRATION NUMBER: 33,692
                                                                                                                                                                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Van Dyk, Tina K.
APPLICANT: LaRossa, Robert Alan
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               REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
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                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: A Facile Method for TITLE OF INVENTION: Identifying Regulated
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                                                                                                                                                                                                                                                                                            STATE: [
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                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                      SOFTWARE: MICROSOFT WORD 2.0C
                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
                                                                                                                                                                                                                                         MEDIUM TYPE:
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REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9989
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GLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/735,545
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                                                                                                                                       FILING DATE:
                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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TELEFAX: 302-773-0164
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302-773-0164
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                                                                                                                                                      US/09/449,083
                                                 CR-9989
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RESULT 17
US-08-286-819A-18
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Patent No. 5871910
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Matches 15; Conservative (
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM MEDIUM TYPE: Floppy
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ORIGINAL SOURCE:
                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5871910
REGISTRATION NUMBER: 24,
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                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                APPLICATION NUMBER: PCT/FR/91/00855 FILING DATE: 29-OCT-1991
                                                                                                                                                                                                                                                                                                                           FILING DATE: 28 CLASSIFICATION:
                                                                                                                                           APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 10-AUG
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Arlington
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                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                             CLASSIFICATION: 435
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(703) 413-2220
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IBM PC compatible
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                 (703) 413-3000
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10-AUG-1992
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HER: 660-060-0 PCT
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                                                                                          FILING DATE: $1-00T-1990
ATTORNEY/AGENT INFORMATION:
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                                          REFERENCE/DOCKET NUMBER: 660-060-0 PCT
                                                        NAME: Oblon, NO. 6013508man F. REGISTRATION NUMBER: 24,618
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FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                  APPLICATION NUMBER: FR 9013579
                                                                                                                                                                                        APPLICATION NUMBER: PCT/FR/91/00855
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
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OPERATING SYSTEM: PC-DOS/MS-DOS
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hes 15; Conserv
                                                                                                                              FILING DATE:
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REFERENCE/DOCKET NUMBER:
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                              Oblon, No. 5871910man F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08286819A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2964 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLINAS, CATHERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COURVALIN, PATRICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                           31-OCT-1990
                                                                                                                               29-OCT-1991
                                                                                                                                                                                                                                                                   28 - DEC - 1993
                                                                                                                                                                                                                                                                                                                                      05-AUG-1994
                                                                                                                                                                                                10-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYPEPTIDES IMPLICATED IN THE EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.7%; Score 15; DB 3; Length 2964; 100.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                     US 08/174,682
                                                                                                                                                 PCT/FR/91/00855
                                                                                                                                                                                                                    US 07/917,146
                                                                                                 FR 9013579
                                                                                                                                                                                                                                                                                                                                                      US/08/286,819A
                24,618
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660-060-0 PCT
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08-08-980-357-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/08980357 Patent No. 6013508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE FITTE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS NUMBERS OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DUKTA-MALEN, SYLVIE APPLICANT: MOLINAS, CATHERINE APPLICANT: COURVALIN, PATRICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 6013508man F.
REGISTATION NUMBER: 24,618
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 00 FILING DATE: 28-DEC-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0)
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
                                                                                                                                                FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS,MS-DOS
SOFTWARE: Patentin Kolease #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. SIREEI: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arithmeton STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                           FILING DATE:
                                                                                                                                APPLICATION NUMBER: FR 9013579
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
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10-AUG-1992
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                     660-060-0 PCI
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Best Local Similarity 100.0%;
Matches 15; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 948-9751 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                             TOPOLOGY: 110-644
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1115 ACAAAACGGTAAAAA 1129
                                                                                                                                                 ORGANISM: Actinobacillus pleuropneumoniae
STRAIN: HV114 (serotype 3 tield strain)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 948-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/01
FILING DATE: 09-APR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Segers, Ruud P.A.M. APPLICANT: Frey, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                  FEAIURE:
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  OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                              LOCATION: 156
                                                                                                                                                                                                                                                                                                      LENGTH: 7004 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gormley, Mary E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300 Piccard Drive, Suite 206 CITY: Rockville
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TYPE: nucleic acid
STRANDEDNESS: double
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TELEX: 248855 OPAT UR
                                                                                                                                   CLONE: PROK5
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                                                                                                                                                                                                                                                                  DNA (genomic)
/function= "RTX-toxin"
/product= "ApxIV_var3"
/gene- "apxIV_var3"
                                                            /codon_start= 1566
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16;
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US-09-057 570:3

Length 10851;

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RESULT 22
US-08-286-819A-16/c
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US-08 286-819A-16
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                                                                                                                         INFORMATION FOR SEQ ID NO: 16:
                 MOLLECULE TYPE:
                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 31-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/174,682 FILING DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                 STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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                                   ToPoLoGY: unknown
                                                                       HAAI.
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                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
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                                                                                                                                        248855 OPAT UK
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                                                                                   10851 base pairs
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               DNA (genomic)
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Best Local Similarity
Matches 15: Conserv
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                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                    SEQUENCE CHARACTERISTICS:
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FILING DATE: 29-OCT-1991
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                                  TOPOLOGY:
                                                     STRANDEDNESS:
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1755 S. Jetterson Davis Highway, Suite 400
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                                  UWCOMIL
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IBM PC compatible
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               DNA (genomic)
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100.0%;
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Pred. No. 14;
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US-08-459-064B-34/c
: Sequence 34, Application US/08459064B
: Patent No. 5747452
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: Goring, Daphne
TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
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HYPOTHETICAL:
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LOCATION: 1..24
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STRANDEDNESS: single
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TRATION NUMBER: 32,167
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100.0%; Pred. No.
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US-08-460-421A-34/c
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GENERAL INFORMATION:
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Patent No. 5837813
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MEDIUM TYPE: Floppy disk
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FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 01-JUN-19
CLASSIFICATION: 514
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                        APPLICANT: RUOSLAHTI, ERKKI I. APPLICANT: MORLA, ALEX TITLE OF INVENTION: FIBRONECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                     TITLE OF INVENTION: MODULATING FIBRONECTIN EXTRACELLULAR MATRIX ASSEMBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CAMPBELL, CATHRYN A. REGISTRATION NUMBER: 31,81 REFERENCE/DOCKET NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/829,462
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    COUNTRY:
                     STATE:
                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: circular
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                            ADDRESSEE:
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                                        SAN DIEGO
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                     CALIFORNIA
                                                           4370 LA JOLLA VILLAGE DRIVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4370 LA JOLLA VILLAGE DRIVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   619-535-8949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MORLA, ALEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RUOSLAHTI, ERKKI I.
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UNITED STATES
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                                                                            CAMPBELL & FLORES LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.2%; Score 14; DB 1; Length 39; 100.0%; Pred. No. 1e+02;
                                                                                                                                                          FIBRONECTIN BINDING SITES AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/340,812
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CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

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; Patent No. 5824519
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Hest Local Similarity 100.08; Prod. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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APPLICATION NUMBER: US 07/829,462
                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NORRIS, JAMES S.
APPLICANT: CLAWSON, GARY A.
TITLE OF INVENTION: TISSUE SPECIFIC AND TARGET RNA SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                              ADDRESSEE: NEED STREET: 127 Pea CHTY: Atlanta
                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                  CLASSIFICATION:
                                       FILING DATE:
                                                                                             SOFTWARE:
                                                                                                                                                   HEDIUM TYPE:
                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                               STATE:
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FILING DATE: 17-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                       APPLICATION NUMBER: US/08/554,969F
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                                                                                                                                                                                                                               Georgia
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                                                                                                                                                                                                                                                                    127 Peachtree Street, Suite 1200
                                                                                               Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                     NEEDLE & ROSENBERG, P.C.
                                                                                                                                                     Floppy disk
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N: 530
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TOPOLOGY: US-08-858-207A-149
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Query Match
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Matches 14: Conservative
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                                                                                                                                        INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hodgson, John APPLICANT: Knowles, David
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                            FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                         NAME: Gimmi, Edward R
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 09-MAY-1997
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                                                                                                    TENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PA
                                                                                                    1037 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            709 Swedeland Road
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                                                    linear
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100.0%; Pred. No.
21.2%; Score 14; DB 4; Length 1037;
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Best Local Similarity

100.0%;

Pred. No.

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                                  us-08-332-576-
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                                                       RESULT 31
Sequence 1, Application US/08332576 Patent No. 5756105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Schardl, Christopher L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09518657 Patent No. 6335188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09518657 Patent No. 6335188
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
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                                                                                                                                                                                                                      Ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/518,657 CURRENT FILING DATE: 2000-03-03 EARLIER APPLICATION NUMBER: 60/125,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/518,657
CURRENT FILING DATE: 2000-03-03
EARLIER APPLICATION NUMBER: 60/125,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schardl, Christopher L. APPLICANT: Wang, Jinghong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Jinghong IIILE OF INVENTION: Endophyte Ergot Alkaloid Synthetic Compounds. Compounds TITLE OF INVENTION: Which Encode Therefor and Related Methods FILE REFERENCE: P-1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: P-1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Endophyte Ergot Alkaloid Synthetic Compounds, Compounds TITLE OF INVENTION: Which Encode Therefor and Related Methods
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                              EAKLIER FILING DATE: 1999-03-22
                                                                                                                                                                                                                                                                                                    ANG : BAAL
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                                                                                                                                                                                                       21.2%; Score 14: DB 4; Length 1598; 100.0%; Pred. No. 59;
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PCT-US95-13672-1
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                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9513672
GENERAL INFORMATION:
APPLICANT: Weiser, Jeffrey M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 21.2%;
Best Local Similarity 100.0%;
Matches 14; Conservative
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               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
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LENGTH: 2100 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                            CITY: Philadelphia
STATE: PA
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ADDRESSEE: Norris
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APPLICATION NUMBER:
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215-568-3439
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PCT/US95/13672
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CLASSIFICATION:

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US-08 188-582-4/c
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Patent No. 5534410
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                              COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IMM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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NAME: OSMBO, Richard A
REGISTRATION NUMBER: 46,627
REPERRENEE/DECKET NUMBER: A.57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
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                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
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TELEPHONE: 215-568-3100
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                                                                                                                                                                                                                                                         STREET: 4 mm.
CITY: San Francisco
STATE: California
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                                                                                    CLASSIFICATION:
                                                                                                    FILING DATE:
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                                                                                                                   APPLICATION NUMBER:
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Comai, Lucio
Dynlact, Brian D.
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Tanese, Naoko
                                                                                                                                                                                                                                                                                                                                                                                                               Weinzierl, Robert O.J.
                                                                                                                                                                                                                                                                                                                                                                                                                             Wang, Edith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoey, Timothy
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US-08-188-582-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-646-715-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 21.2%; Score 14; DB 1; Hest Local Similarity 100.0%; Pred. No. 56; Matches 14; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                   TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: UCCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bynlact, Brian D. APPLICANT: Hoey, Timothy APPLICANT: Rupport, Siegfrie APPLICANT: Tanese, Naoko
                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                      FILING DATE: 28-JAN-1994
AUTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tjian, Robert APPLICANT: Comai, Lucio
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                                                                                                                                            TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 09-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
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STRANDEDNESS: double
TOPOLOGY: linear
                    STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2359 base pairs
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                                                             LENGTH: 2359 base pairs
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                                    nucleic acid
                                                                                                                                                                                                                                                  Osman, Richard A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
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(415) 398-3249
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US-08-646-715-4
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Best Local Similarity 100.0%; Pred. No.
Matches 14; Conservative 0; Mismatc
                                   Matches
                                                  Query Match
Best Local Similarity
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FELEFAX: (301) 948-9751
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6736 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Seqers, Ruud P.A.M.
APPLICANT: Erey, Joachim
TITLE OF INVENTION: Live attenuated /
TITLE OF INVENTION: pleuropneumoniae
NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                   OTHER INFORMATION:
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                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Akzo l
STREET: 1300 Pice
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 157
                                                                                                                                                                                                                                                                                           ORGANISM: Actinobacillus pleuropneumoniae STRALN: 4074 (serotype 1 reference strain)
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                                                                                                                                                                                                                                                                                                                                                              FOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
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29 TAAAAAAGCGGTAG 42
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                                   14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                                                                                                             1576.
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09-APR-1998
 21.2%; United No. 100.0%; Pred. No. Nismatches
                                                                                                                                                                                                           . 6549
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                                                                                                                   /function= "RTX-toxin"
/product= "ApxIV_varl"
/gene= "apxIV_varl"
/number= l
                                                                                                                                                                                        /codon_start= 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6013266el Patent Department
                                                  Score 14: DB 3; 
; Pred. No. 48;
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. 56;
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                                 0;
                                                               Length 6736;
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                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 948-7400
TELEFAX: (301) 948-7951
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN: Actinobacillus pleuropneumoniae STRAIN: 4074 (serotype l reference strain) IMMEDIATE SOURCE: CLONE: pROK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
              FEATURE:
                                                                                                                                                                                                                                      OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 6736 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-APR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: Akzo No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Live attenuated a TITLE OF INVENTION: pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Segers, Rund P.A.M. APPLICANT: Frey, Joachim
                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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                                OTHER INFORMATION: /standard_name OTHER INFORMATION: /label= -10_s
                                                                                                                    OTHER INFORMATION:
                                                                                                                                                      OTHER INFORMATION
                                                                                                                                                                   LOCATION: 1..453
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1132..6549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
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                                                                    LOCATION:
                                                                                   NAME/KEY:
                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD:
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617..623
-35_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double
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                                                  /standard_name= "-10"
                                                                                                                                                                                                                                                                                                       /codon_start= 1132
/function= "RTX toxin"
                                                                                                                                                  /label- mrp
                                                                                                                                                                                                                                                    /qene= "Apx1V_v1"
                                                                                                                                                                                                                                                                       /product= "ApxIV"
/evidence= EXPERIMENTAL
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                                                                                                                                    /standard_name= "mrp"
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; Sequence 3, Application US/09150805; Patent No. 6140080
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                                                     RESULT 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/08477451 Patent No. 5928865
                                                                                                                                                                             Matches
                                                                                                                                                                                            Overy Match 21.2%; Score 14; DB 2; Length 19932; Best Local Similarity 100.0%; Pred. No. 41;
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CHRRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                      829 TANANANGOGOTAG 842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                         29 TANAAAAGCGGTAG 42
                                                                                                                                                                                                                                                                                   Topology: linear
                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                       LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McClung, Barbara G. REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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US-09-150-805-13
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Matches 13; Conserv
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MEDIUM TYPE: Floppy
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                                                                                                              TITLE OF INVENTION: PROMOTER ELEMENTS CONFERRING TITLE OF INVENTION: ROOT-PREFERRED GENE EXPRESSION
                                                                                                                                                      APPLICANT: Bruce, Wesley APPLICANT: Lu, Guihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid pescription: /desc - "oligonucleotide"
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NAME: Yates, Michael E.
REGISTRATION NUMBER: 36,
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                                                                          CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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                                                                                                 NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
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STRANDEDNESS: single
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                STREET:
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                   BCX 1000
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(515) 248-4844
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100.0%; Pred. No. 3.7e+(
rative 0; Mismatches
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RESULT 40
US-08-996-069A-3
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                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bruce, Wesley
APPLICANT: Lu, Guihua
TITLE OF INVENTION: PROMOTER ELEMENTS CONFERRING
TITLE OF (NVENTION: ROOT-PREFERRED GENE EXPRESSION
NUMBER OF SEQUENCES: 19
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LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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FILING DATE: 22-DEC-1997
APPLICATION NUMBER: US 08/649,172
FILING DATE: 17-MAY-1996
AITORNBY/AGENT INFORMALION:
NAME: VALES MICCHAEL
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                                      CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
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FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                               ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O. STREET: Box 1000 CITY: Johnston
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPAX: (515) 248-4844
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                                                                                                    FILING DATE:
                                                                                                                      APPLICATION NUMBER:
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100.0%; Pred. No. 3.7e+02;
                                        US 08/649, 172
                                                                                                                        us/08/996,069A
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US-08-996-069A-13
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                                                                                                            TELEFAX: (515) 248-4844 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bruce, Wesley
APPLICANT: Lu, Guihua
TITLE OF INVENTION: PROMOTER ELEMENTS CONFEREING
TITLE OF INVENTION: ROOT-PREFERRED GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Yates, michael E.
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Darwin Bu
STREET: Box 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..18
OTHER_INFORMATION: /product= "N7913"
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Johnston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                    TOPOLOGY:
                                  STRANDEDNESS:
                                                                        LENGTH:
                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/649,172
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                  nucleic acid
EDNESS: single
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                                                                      18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Darwin Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : (515) 248-4800
(515) 248-4844
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                    Tinear
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                                                                                                                                                 (515) 248-4800
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DNA (genomic)
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Patent No. 6077992
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EARLIER APPLICATION NUMBER: 60/063,504
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TITLE OF INVESTIGN: BINARY VIRAL EXPRESSION SYSTEM IN PLANTS
FILE REFERENCE: CL-1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Word Version 7.0A
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              TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8991
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       STREET: 60 L.
CITY: Minneapolis
                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 07-JU
                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                       REFERENCE/DOCKET NUMBER: MED1003USD4
                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                          HEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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80 S. 8th Street, Suite 1902
612 334 8994
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                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                     07 - JUN - 1995
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100.0%; Pred. No. 3.6e+02;
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                                                                          30,099
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US-08-480-173A-26/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                TELEPHONE: 612-334-899
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas F
REGISTRATION NUMBER: 30,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
PEATURE
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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                                                                                       FEATURE
                                                                                                         MOLECULE TYPE: DNA (synthetic)
               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: single-stranded "sticky end""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_teature LOCATION: 1..4
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                                                    LOCATION;
                                                                                                                                          STRANDEDNESS:
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                                                                    NAME/KEY: misc_teature
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                                                                                                                          : ASOTOdo.I.
                                                                                                                                                                               LENGTH:
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                                                                                                                                                                             24 base pairs
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80 S. 8th Street, Suite 1902
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100.0%; Pred. No. 3.7
Mative 0; Mismatches
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               /note- "Nucleotides 1-4 form a single-stranded "sticky end""
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                                                                                                                                 US-08-484-408A-25
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Patent No. 6117653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.7%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 3.5 Matches 13; Conservative 0; Mismatches
                                                            Matches
                                                                          Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: POPOVICE, Thomas E
RECISTRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MEDIO03USD4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8991
TELEPAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSIKE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thoma, Hans A
TITLE OF LUVERTION: HEPATITIS B SUNFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (synthetic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                               LOCATION: 5..24
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                        hes 13; Conserv
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "Nucleotides 1-4 form a OTHER INFORMATION: single-stranded "sticky end""
                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: 5..24
                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..4
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
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3 AGATCTGGATCCG 15
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                                                                                                                                                                                                                                                                                                                                                                               linear
                                                    19.7%; Score 13; DB 3; Le 100.0%; Pred. No. 3.5e+02; O: Mismatches 0;
                                                                                                                                             /note= "Adapter sequence results
from oligonucleotide duplex formation with nucleotides 5-24
SEQ 1D NO: 26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Adapter sequence results from oligonucleotide duplex formation with nucleotides 5-24 SEQ 1D NO: 25"
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Db 6 AGATCTGGATCCG 18

Search completed: November 5, 2002, 08:26:11 Job time: 37.2973 secs

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RESULT 45
AX144614
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TITLE
JOURNAL
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Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                             Query Match
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                                                                              2668 TAAAAAAGCGGTAGAT 2683
                                                                                                                     29 TAAAAAAGCGGTAGAT 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis nucleic acids and proteins Patent: WO 0134809-A 3924 17-MAY-2001; GLAXO GROUP LIMITED (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimmerly, W.J
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Staphylococcus epidermidis
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF269294 3246 bp DNA linear BCT (Staphylococcus epidermidis strain SR1 clone step.1000c01
                                                                                                                                                                                                                                                                                                                                                                                                    Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5
Drive, Research Triangle Park, North Carolina 27709-3398, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-MAY-2000) Departments of Genomic Sciences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Furdon, P.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taylor,J.D., Kimmerly,W.J., Nelsen,A.J., Godlevski,M.M., Rubino,M.A., Nelson,F.J., Rivers,P.R., Torrucilla-Miller,I., Expherd, N.S., Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shephord,N.S., Fleming,T., Guan,X., Du,I., Cain,D.H., Miller,G.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimmerly,W.J., Taylor,J.D., Nelsen,A.J., Godlevski,M.M., Rublio,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I., Eistenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N.S., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Staphylococcus group; Staphylococcus. 1 (bases 1 to 3246)
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                                                                                                                                                                                                                                                           /organism="Staphylococcus epidermidis"
/strain="SH1"
/db_xref="traxon:1282"
/cione="step.1000c01"
a 533 c 536 g 1086 t
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/db_xcef="taxon:32630"
/note="synthetic nucleic acid sequence"
1 600 c 422 g 1071 t
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100.0%;
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TITLE
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Best Local Similarity
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                                                         2668 TAAAAAAGCGGTAGAT 2683
                                                                                      29 TAAAAAAGCGGTAGAT 44
                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3336 from Patent WO0134809
AX144614
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                                                                                                                    Conservative
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/db_xref="taxon:32630"
/notee="synthetic nucleic acid sequence"
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AUTHORS
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AUTHORS
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Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-MAY-1996) Fumio Osaka, National Institute of Genetics; IIII Yata, Mishima, Shizuoka 411, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   usaka, F
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3 (bases 1 to 161
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Mol. Cell. Biol. 17 (6), 3388-3397 (1997)
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A mbiquitin-conjugating enzyme in lission yeast that is essential
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1015. .106
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/protein_id "BAA20375.1"
/db_xref "GI:2190255"
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/qene.*ucbP4**
/mate.**
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/qene="ucbp4"
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TPG1SAFPDSDSNILHWAGTITGPSDTYYFGLKFKISMSFPANYPYSPPTITFTSPMW
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/codon_start-1
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/yene="ucbP4"
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synthetic construct artificial sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taylor, J.David., Kimmerly, W.J., Nelsen, A.J., Goddlevski, M.M., Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I., Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kimmerly,W.J., Taylor,J.David., Nelsen,A.J., Godlevski,M.M., Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I., Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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AX145202
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                                                                                                                                                                                                                                                                                                                                                                                   /organism~"Staphylococcus epidermidis"
/strain-"SRI"
/db_xret--ftaxon:1282"
/ctone-"step.1028c03"
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Havelund, S., Halstr.o slashed.m, J.,
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Sequence 2 from Patent W00124811.
AXI05687
AXI05687.1 G1:13921709
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Fraser,C.M., Venter,C., Tuemmler,B., Hoheis
Hilbert,H., Timmis,K.N., Moore,E., Straetz,
Dna sequences which code export systems
Patent: WO 0107591-A 21 01-FEB-2001;
THE INSTITUTE FOR GENOMIC RESEARCH (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               April receptor (bcma) and uses thereof Patent: WO 0124811-A 2 12-APR-2001; BIOGEN, INC. (US) : Apotech R&D S.A. (CH)
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Sequence 21 from Patent W00107591.
AX079100
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Schneider, P., Thompson, J., Cachero, T.,
                           Yeast chkl and ucbP4 DNA, partial D85545
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UcbP4; ucbP4; protein kinase; chkl
                D85545.1 GI:2190253
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AR151513
                                                                                                                                                                                                              Adylated insulin
Patent: US 5750497-A 40 12-MAY-1998;
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layelund,S., Halstr.o slashed.m,J., Jonassen,L., Andersen,A.Sloth.
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                                                                                                                                                                                                                                                                                                                                          Sequence 40 from patent AR007430
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Kmiec, E.B., Holloman, W.K. and Gerhold, D.
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Pred. No. 60;
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l (bases 1 to 523)
Havelund,S., Halstr.o slashed.m,J.,
and Markussen,J.
Acylated insulin
Patent: US 5750497-A 43 12-MAY-1998;
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Sequence 19 from patent US 5750497.
ARO07416
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                                                            Unclassified
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                                                                                                                       Sequence 43 from patent US 5750497 AR007432
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Havelund,S., Halstr.o slashed.m,J.,
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and Markussen,J.
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ilarity 100.0%;
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                                                                                                                                                                                                                                                      Conservative
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101 c 104 g
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103 c 101 g
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1. .523
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                                                                                                           GI:3966916
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Pred. No.
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                                     Jonassen, I.,
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                                       Andersen, A. Sloth
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                                        contains three domains; as 1-90 contains three membrane spanning domains; as 90-780 is non-membrane, and as 780-1081 contains ten possible membrane spanning domains. Some similarity in C-teminal membrane domain to eukaryotic proteins e.g. CCSA_CHLKE cytochrome C biogenesis protein C biogenesis protein C biogenesis protein C biogenesis protein C biogenesis cytochrome C biogenesis protein C biogenesis 
                                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"Cj1013c"
complement(3961..7206)
/gene-"Cj1013c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="putative membrane protein"
/protein_id="CAB73268.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(3495. .3944)
/qene="Cjl012c"
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/trans1_table=11
/product="putative membrane protein"
/protein_id="CAB73267.1"
/db_xref="G1:6968447"
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2596. .3363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \tt GGLSVGEENALMYETVONLNPYLDENRPRYLMGVGTPEDLVENVERGVDMFDCVMPTRNARNGTFFTSFGKFNLKKAEFINDHEVIDSTCSCYTCRNFSRGYLNHLFKAKELTFFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="queuine tRNA-ribosyltransferase"
/protein_id="CAB73266.1"
/db_xref="G1:6968446"
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TGT_ECOLI queuine tRNA-ribosyltransferase (EC 24.2.29)
(375 aa), fasta scores; opt: 1016 z-score: 1190.9 E(): 0,
41.3% identity in 373 aa overlap. 56.7% identity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="C]1010, tgt, probable queuine
/note="C]1010, tgt, probable queuine
+ewa-ribosvitransferase, len: 373 aa; similar to many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="tgt"
/EC_number="2.4.2.29"
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1473. .2594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (3961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKFDTDLDKMIIASSDVKLTDIELKELAKLYVQTHKLGSKTSKELDEAAKKKLEEVSA
LAANINASAQTVSYLNKELKKIYGSYKKEIDAYEHMGLAKRKIKEDK"
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3416. .3492
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/transl_table=11
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1473, .2594
prokaryotic equivalents e.g. CCMF_ECOLI cytochrome C-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAB73268
/db_xref="GI:6968448"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hp match"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /qene="Cj1012c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="tRNA-Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"tRNA Arg anticodon GCG, Cove score 83.29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="tRNA-Arg"
                                                                                                                                                                                                                                                                                                                                                                     /note="Cj1013c, probable membrane protein, len: 1081 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MVIFCAALALLLFLGVIAYLITSDGKKTIKKQKTSQKQHVAEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 3492
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AVLKYKDLĪLNAHYTYKENNNSDPLLVLMLSOKGSOGVIVKFEKGEVKNIEGVNFAFM
KNOKKAPFVKIDERUTILSSENLHFLSKLDGCONLDLKIEGERANAKERILVEI NOISFV
VKAASLHAQEALEGGENGQDESFWLHFKSAMLLEVGREFMLISTEGEPONKKSLLLHFK
DFALSNENKNIELTGSNALKLELSYKNESKEPYIFEYNKFIMIELADQKFFISMALSY
EQLIPFOLYLDRYPODESFWLHFKSAMLEVERGYKIFFOYRIFMNVLLDYDGYRFYQ
SSYDQDEKGTYVLDRYPOSMSPASYASEITVKNNNKHPFOYRIFMNVLLDYDGYRFYQ
SSYDQDEKGTYLSVKNOCKIFYIGYELLCIGMFWNFLLRHSRERTLARILKNOTLK
HTSVIIFILLSEGSEKTFAQDLNSTLEVVNTNHAKALATILIVQKSADGRMVPFDTLS
REILEKIHGSDSYKGONSNAVMLSMLVDVDKWOLEPFILMPONGAVEDALANLLEIPS
AKYIAYKDFEDENNRYKLOKYVENAMLKNDNAFGVEDKEILKDEKANVVNLUFYGGEL
KFIRFYODEKIGYKMPSKIKUBMEITSNKREIFVKLAPVYLAGFLLLILVFSGEL
KFIRFYODEKIGYKMPSKIKUBMEITSNKREIFVKLAPVYLAGFLLLILVFSGEL
KFIRFYODEKIGYKMPSKIKUBMEITSNKREIFVKLAPVYLAGFLLLILVFSGEL
KFIRFYODEKIGYKMPSKIKUBMEITSNKREIFVKLAPVYLAGFLLLILVFSGEL
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233 aa overlap No Hp ortholog. Contains PS00017
237 ATP/STP-binding site motif A (P-Lop), PS00211 ABC
                                /note-"CJ1015c, livG, probable branched-chain amino-acid ABC transport system ATP-binding protein, len: 256 aa; similar to e.g. LIVG_ECQLI high-attinity branched-chain amino acid transport ATP-binding protein (255 aa), fasta scores; opt: 680 z-score: 800.2 E(): 0, 41.2% identity in 250 aa overlap. No HP ortholog. Contains PS00017
ATP/GTP-binding site motif A (P-loop), PS00211 ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7482...7526)
/gene-"livf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(7299. .7841)
/gene-"livf"
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/product="branched-chain amino-acid ABC transport system
/probleman protein"
/protein_id="CAB73270.1"
/db_xref="G1:6968450"
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/gene="livf"
complement(7224..7919)
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/protein_id="CAB73269.1"
/db_xref="GI:6968449"
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                                                                                                                                                                                                                                                                                                                                      complement(7906. .8676)
/gene="livG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="PS00211 ABC transporters family signature"
complement(7797, .7820)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Pfam match to entry PF00005 ABC_tran, transporters, score 147.40, E-value 2.5e-40"
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IGDDEIRKKYLGL"
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Nallnsvkrtgevnflgydtkrhlthtly¢kgialvpegrrvfinlsveenlkigafn
Naenyehlreûmyklfprlaskkhalagtlsgghaūmiaishalmsepkllmidepsl
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TLPTREHTQNSLTESSKTSLRTSATKDGERYSAVNDRYTGNLPFANSFKLKLNLGDDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (7906. .8676)
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Basham,D., Chillingworth,T., Davies,R.M., Feltwell,T., Holro
Jagels,K., Karlysbev,A., Moule,S., Pallen,M.J., Penn,C.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quail, M., Rajandream, M.A., Rutherford, K.M., VanVliet, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 282183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 282183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-182A20"
                                                                                                 SSEYTDI.HYFDPTSTARI.ENIMSKDFKQAFTYMQDEFETKKSYEAI.KSI.NPNI.ETETM
DEWGI.SVNDTHANLADARMTI.SRREMDEL.PDIALTAQYTGI.GVGETMEVKTPAGSTFA
                                                                                                                                         /product="bypothetical protein 0]1009c"
/profein_id="0AB73265.1"
/db_xref="0.1696845"
/translation="munifildBiliAKHFLERICFEKGLGYFFTVV0QUSEKUNLNI
                                                                                                                                                                                                                                                                                              /qene="Cj1009c"
complame="
                 KIKKLSEDKEGVFFOYFNIDFKOISMMLONNDIGLVVIDIKNFEKEKOAFFDLKIPIN
KVGEASFDELKEAIILSADESFLENNANVIIDLSKOLDFGVILYYYNPNSONIIDMEE
                                                         YRH ISS IQQKRWRIYL IYRNSK IYFYKPSFYLEPNDS LLIVGDPYVIQS IFHNIRGKA
GQFPMPFGSNYFALIDMKNMNQNMQERVIJYTYLKLYYQKSNAKRFFIHYINPKLGVMYE
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Y FRSESKEY DKNIQ I INKNDENPLENEQY REDELQ FYSFQKELLNRDFARNESTNENF
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                                                                                                                                                                                                                                                                                          /note="C)1009c, unknown,
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                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="NCTC 11168"
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100.0%; Prod. No. .
Thive 0; Mismon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jejuni sequencing at the Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Centre, Wellcome Trust Genome Campus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are available
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FEATURES
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           Elhaj C., Escotto, M., Palls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garcia, N., Gill, R., Gorrell, J.H., Guevera, W., Gunbrathe, P., Hale, S., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Univet, S., Jackson, L.E., Jacobson, B., Jia Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, B., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, B., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, B., King, L., Lowis, L.C., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lu, X., Lucler, R., Luna, R., Louiseged, H., Lozado, R.J., Lu, X., Lucler, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuon, G., Oradunye, N., Oviedo, R., Pace, A., Payton, B., Peery, L., Peters, L., Pickens, R., Primus, E., Pull, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   available and the accession number will be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/chromosome="2"
/clone="GJ1267_F10"
4 32642 c 32750 g 52239 t
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Peters, L., Pickens, R., Primus, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Edgar, D., Edwards, C.C.,
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Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.

bp in length

SOURCE

ORIGIN

COMMENT

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REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruiz,S., Savery,G., Schcrer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaiko,T., Sparks,A., Stanley,H., Sisson,H., Sutton,A., Svatck,A., Tabor,P., Tamerisa, K. Tang,H., Iansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Verz,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Walliams,G., Williams,A., Wergley,R., Wooden,S., Walliams,G., Williams,G., W
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Direct Submission
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NOTE: This is a 'working draft' sequence. It currently
consists of 51 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hqsc-help@bcm.tmc.edu
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             Submitted (22-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:Isasaki@hlas.affrc.qo.jp, URL:http://iqp.dna.affrc.qo.jp/.Tel:81-298-38-7441, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by
                                                                                                                                            Published Only in Database (2001) In press 2 (bases 1 to 163156) Sasaki,T., Matsumoto,T. and Yamamoto,K.
                                                                                                                                                                                                      Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DM
clone:OJ1267_F10
                                                                                                                                                                                                                                                         Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Podics; Podceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 163156)
                                                                                                                                                                                                                                                                                                                                     Oryza sativa
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Oryza sativa (cultivar:Nipponbare) DNA, clone:0.11267_F10
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combining Monsanto and RGP-Japan sequencing data
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hes 17; Conser
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                                                                                                                                                                                             Rattus norvegicus clone CH230-114N22, ***, 71 unordered pieces.
                       Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
                                                           Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.
                                                                                                                                           Rattus norvegicus
                                                                                                                                                        Norway rat.
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                                                                                                                                                                                  AC106377.1 GI:18138898
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                                                   Benton, J., Bimage, K.,
                                                                                                                 Mammalia; Eutheria;
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Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
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50279: contig of 707 bp
50379: gap of 100 bp
50379: contig of 714 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44678: gap of
45394: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43854: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51193: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47157: gap of 47879: con
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                                                                                                                               Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53615:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52799: gap of 100 bp 53515: contig of 716 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48760: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47979: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46325:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45494:
           Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.
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100.0%; Fi
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                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                          Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 727 bp in
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contig of 703 bp
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                                                   Blankenburg, K., Bonnin, D., Bouck, J.
                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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SEQUENCING IN PROGRESS
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Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Sitone,H., Sutton,A., Svatck,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telirod,B., Thomas,K., Taylor,C., Taylor,T., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Walliams,G., Williams,G., Walliamson,A., Wileczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G., and Gibbs,R.
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Joudah, S., Karisson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C.,
Kovar, C., Kratovic, J., Kureshi, A., Lucier, R., Luna, R.,
Kovar, C., Kasey, E., Masey, B., Martindale, A.,
Ma, J., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Lu, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Consensus quality: 114472 bases at least Q40 consensus quality: 124676 bases at least Q30 consensus quality: 133577 bases at least Q30 Estimated insert size: 117794; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-ip estimation Quality coverage: 1.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap: version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: CH230-114N22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosetti, M., Roy, A., Santos, R., Schauer, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 will be sequenced to completion. In the event that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the record is updated, the accession number will
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-----Project Information
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2591: qap of 100 bp
26704: contig of 713 bp in
26804: qap of 100 bp
27524: contig of 720 bp in
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12161: contig of
38159: gap of
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18607: contiq of 719 bp in
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24300: contid of 721 bp
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10521: contig of 687 b
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/product="tRNA-Leu"
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/protein_id-"AAL64874.1"
/protein_id-"AAL64874.1"
/db_xref-"Gi:1816.603"
/translation-"MRVLVKIFGPKYFGLDTYDVITLVLDLKEGATVGDVWEELEKRY
PGLRQKLLRGEEIIPMHDIWVNGRSIYFLQGLKTALAEGDVVQITPPFGG"
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NRASDETTGLNRPAPRKRPSHTLSAVVMVKEGFAWAI.GASAGHYRPAIYAQLIQNVIW
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/note="Biosynthesis of carriers; Glutathione"
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/db_xref="G1:18161604"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(6049
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5768. .6052
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/gene="PAE3373"
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∕qene="PAE3373"
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LPHLGGVGGDFLAVVHKGDRAESVLGLGWAPRKIPDRPPRRGIQSAVVPGYIAGLVEF
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                                                                                                                                                                                                    LLRGLKSLG1KPSE1TKVF1THYHADHTTLAQFIAEVASPDFYIGEGEVSEVATSFED
LARLYAEEYRRHGAPAEVAEAFLKTHPMSRYNKAFEDVWKLPWKRVKDGELLDCGLKA
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  Birren, B., Linton, L., Nusbaum, C
Mus musculus, clone RP23-2071.14
                                      Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
1 (bases 1 to 56766)
                                                                                                                                                                   AC107757
AC107757.1 GI:18308459
                                                                                                                                                                                                           AC107757 55766 bp DNA linear HTG 24-JAN-2002 Mus musculus clone RP23-207L14, LOW-PASS SEQUENCE SAMPLING.
                      Birren, B.,
                                                                                                        Mus musculus
                                                                                                                                                   HTG; HTGS_PHASEO.
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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8846.,9430
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complement(7956. .8807)
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/note="Hypothetical; Conserved"
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AALIVLRPGGGYLGLTDVYVDIRVDDHPDPVAELKRIFKIMELTLLQREDPLDVVLKK
DVAGEVQEALRRIGFYKREPTGVMDEETERAFRNWAGYENFENKIRNDDKIMGSLYRY
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conjectural"
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resistance"
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PGRLRELLEPGAKIWARRTVRGRTEYYLAAVELDDELVLVDSSLHNKIAVWELENGYE
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                    Nusbaum, C.
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                                   Pyrobaculum aerophilum strain
AE009927.1 GI:18161597
                                                                                                                                                                                                                                                                                                                                PIONEER HI-BRED INTERNATIONAL, INC. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                artificial sequence.
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            AE009441
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4 9 c 9 q 11 t 3
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/db_xref="taxon:32630"
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Direct Submission
Submitted (12-DEC-2001) Microbiology and Molecular Genetics,
University of California, Los Angeles, 405 Hilgard Ave, Los
Angeles, CA 90095-1489, USA
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                                                                                                                                                                                                                                                                                 /product="GMP synthetase (qlutamine-hydrolysing)"
/protein_id="AAL64871.1"
/db_xre1="G1:18161600"
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/protein_id="AAL64870.1"
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Bruce, W.B. and Niu, X.
Novel root-preferred promoter elements and Patent: WO 0153502-A 8 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Novel root-preferred promoter elements and Patent: WO 0153502-A 5 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Sequence 5 from Patent W00153502
AX203097
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synthetic construct
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Bruce, W.B. and Niu, X.
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/db_xref="taxon:33630"
/note="random oligonucleotide"
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/db_xref="taxon:32830"
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Sequence 11 from Patent WO0153502.
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Novel root-preferred promoter elements and methods of use Patent: WO 0153502-A 10 26-JGL-2001;
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/db_xrel="taxon:32630"
/note="primer with BamHI site"
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Bruce, W.B. and Niu, X.
                                                       synthetic construct
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PIONEER HI-HRED INTERNATIONAL, INC. (US)
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Bruce, W.B. and Niu, X.
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Bruce, W. H. and Niu, X.
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/db_xref="taxon:32630"
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Sequence 23 from Patent W00153502
AX203115
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Novel root-preferred promoter elements and methods of Patent: WO 0153502-A 21 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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AX203113
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Bruce.W.B. and Niu.X.

Novel roct-preferred promoter elements and Patent: wo 0153502-A 23 26-JUL-2001;
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                                                                 PIONEER HI-BRED INTERNATIONAL, INC. (US)
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//db_xrei-"taxon:32630"
/note-"synthetic sequences flanking a random oligonuclectide"
a 11 c 21 g 14 t 1 others
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oligonucleotide"
a  12 c  20 g  13 t  1 others
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note="synthetic sequences flanking
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1 (bases 1 to 62)

1 (bases 1 to 62)

Novel rout-preferred promoter elements and Patent: WO 0153502-A 6 26-JUL-2001;

PIONEER HI-BREED INTERNATIONAL, INC. (US)
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Sequence 6 from Patent W00153502.
AXX03098
AXX03098.1 GI:15392457
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Ax203106
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/note="random oligonucleotide"
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1 (bases 1 to 66)
Bruce, W.B. and Niu, X.
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Bruce, W.B. and Niu, X.
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Bruce, W.B. and Niu, X. Novel root-preferred promoter elements and methods Patent: WO 0153502-A 19 26-JUL-2001;
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Bruce, W.B. and Niu, X.
Novel root-preferred promoter elements and methods of use Patent: WO 013562-A 3 26-JUL-2001,
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Patent: WO 0153502-A 1 26-JUL-2001;
PIONDER HI-BRED INTERNATIONAL, INC. (US)
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ilarity 100.0%; Pred. No. 0.00059;
Conservative 0; Mismatcher
50.0%; Score 33; DB 6; Lk
100.0%; Pred. No. 1.4e-09;
                                                                                                                                                                                                                                                                                                                                                                               Novel plant promoters and methods of use
Patent: WO 0153476-A 25 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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                                                                    1 TGAGATCTGGATCCGTTCGACAAAACGGTAAAA 33
                                                                                        1 TGAGATCTGGATCCGTTCGACAAAACGGTAAAA 33
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Sequence 25 from Patent Wc0153476.
AX207072
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Sequence 1 from Patent WO0153502.
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1 (bases 1 to 66)
Bruce, W.B. and Niu, X,
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(bases 1 to 26)

Bruce, W.B. and Niu, X.
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Sequence Sodnones Sequence

AX204107 AX204108 AX204108

AX204116 AX204095 AX207072 AX203093 AX204114 8 AX204115 8

AX204106 AX204098 AX204112 AX204102 AX204103 AX204104

AX204110 AX204111

Sequence

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artificial sequence.

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Bruce,W.B. and Nic 8

Novel root-preferred promoter elements and methods of use Patent: WO 0153502-A 2 26-JUL-2001;

PHONEER HI-BRED INPERNATIONAL, INC. (US)
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//organism="synthetic construct"
/db_xret="taxon:42630"
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and is derived by analysis of the total score distribution.
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AR007430 S AR007416 S

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AK105687 3

40 AUG 2001

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Linear

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AF269884 Staphyloc AX145202 Sequence AF269294 Staphyloc AX144614 Sequence

Sequence

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

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US-09-766-113-2 66 Title: Perfect score:

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99

OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query				
NO.	Score		Match Length DB	DB	ID	Description
	99	100.0	99	22	AAS08433	A plant root-profe
7	99	100.0	99	22	AAS08453	A plant root prefe
~	33		99	22	AAS08434	A plant root-prefe
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26-JUL-2001

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ALIGNMENTS

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Root-preferred promotor element, RPE, abiotic stress, drought, salfnity; pesticide resistance; herbicide resistance; biotic stress; disease resistance; tungal disease parterial disease; viral disease; insert attack; nematode attack; RPEI4; random oligonocleotide library;
                                                                          A plant root-preferred promoter element (RPE), RPE 14.
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/*taq~ c
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                                                                                                                                                                                                                         The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonuclectide library (RGL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonuclectides. I lanked by 5 and 3' llanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonuclectide. The method is used for isolating fissue specific promoters from plants, including but not limited to root specific promoters from plants, including but not limited to root specific promoters from plants, including but not limited to root specific promoters or root-preferred promoter elements (RPE). The RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic
                                                                                                                                                       expression of nucleotide sequences in a plant comprises identifying and isolating dissue-preferred promoter elements
                                                                                                                                                Producing tissue-preferred promoter elements constructs for regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                koot-preferred promoter element, RPE, abiotic stress, drought, salinity; pesticide resistance; herbicide resistance; biotic stress, discase resistance; tungal disease; bacterial disease; viral disease; insect attack; nematode attack; RPE21; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGAGATCTGGATCCGTTCGACAAAAGGGTAAAAAAGCGGTAGATTACCGTCCTACGAATT 60
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                                                                                                                                                                                                                                                                                                                                                                                                     stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 66; DB 22; Length 66; 100.0%; Pred. No. 4.8e-26;
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                                                              (PION-) PIONRER HI-BRED INT INC
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             19-JAN-2001; 2001WO-US02011.
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                                                                                                                   WP1; 2001-442261/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sest Local Similarity
                                                                                           Bruce WB, Niu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAGCTG 66
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61 CAGCTG 66
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concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random olimproficionis, Ilanked by 5° and 3′ ilanking sequences, which hybridise to tissue specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating trissue specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements.
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linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Root-preferred promoter element; RPE; abiotic stress; drought; salinity; pesticide resistance; herbicide resistance; blotic stress; disease; resistance; tunqal disease; bioterial disease; viral disease; linseet attack; nemalode attack; RPE19; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    achieve a desired phonotypic effect, e.g. abiotic stress (drought, temperature, salinity, posticide and herbicide resistance) and biotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the sequence represents a plant root-preferred promoter element, RPE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGAGATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTACGAATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stress (disease resistance, resistance to attack by fundi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated from a random oligonucleotide library (RoL). The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 56; DB 22; Length 56; 100.0%; Pred. No. 4.8e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A plant root-preferred promoter element (RPE), RPE 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 66 BP; 21 A; 14 C; 16 G; 15 T; 0 other;
                                                                       "3'_flanking_sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             viruses, insects and nematodes).
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                                                                                                                                                                                                                                                                                                             19-JAN-2001; 2001WO-US02011.
                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-2000; 2000US-0177473.
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49..66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bruce WB, Niu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CAGCTG 66
                                                                                                                                                      WO200153502-A2
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The sequence represents a plant root-preferred promoter clement, RPE, isolated from a random oligonuclectide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter concerns a method of identifying and isolating tissue-preferred promoter. I lanked by 5' and 3' flanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating tissue-specific promoters from plants, including but not limited to tissue-specific promoters from plants, including but not limited to root-specific promoters from plants, including but not limited to linked to a nucleotide sequence whose expression is to be controlled to a chike to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and hebiotide resistance) and biotic stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                              Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66 BP; 22 A; 14 C; 15 G; 15 T; 0 other;
                                a
"5'_flanking_sequence"
                                                                                                                             /*tag= c
/label= "3'_flanking_sequence"
                                                                            b
"Randomised sequence"
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 Location/Qualifiers
                                                                                                                                                                                                                                                                                                               (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viruses, insects and nematodes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig 1; 45pp; English.
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                                                                                                                                                                                                                                                                                 21-JAN-2000; 2000US-0177473.
                                                                                                                                                                                                                                               19-JAN-2001; 2001WO-US02011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                              49..66
                                                                  9.48
                 1 . . 18
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442261/47
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es 33; Conserv
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                                                                                                                                                                               W0200153502-A2
Key
misc_feature
                                                                  misc_teature
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Matches
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                                                                                                                                                                                                         New plant promoters with synthetic multimeric promoter element regions, useful in plant molecular biology, particularly in regulating gene expression in plants to increase resistance against insects or
                                                                                                                                                                                                                                                                                                            AAH42709-72 represent promoter elements or transcription binding sites.
                                                                                                                                                                                                                                                                                                                                                                   biology, particularly in requiating gene expression in plants. The
promoters are especially useful for transforming plants or plant cells,
e.g. to increase resistance against insects or herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Root-preferred promoter element, RPE; abiotic stress; drought; salinity; pesticide resistance; herbicide resistance; biotic stress; disease; resistance; fungal disease; bacterial disease; viral disease; insect attack; nematode attack; RPE15; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                       They are used to to construct synthetic multimeric promoter element regions (SMPERs). The specification describes plant promoters which comprise SMPERs. The plant promoters are useful in plant molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.4%; Score 26; DB 22; Length 26; 100.0%; Pred. No. 0.00016; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A plant root-preferred promoter element (RPE), RPE 15.
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"5′_flanking_sequence"
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"3'_flanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26 BP; 12 A; 4 C; 6 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 AAACGGTAAAAAAGCGGTAGATTACC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAACGGTAAAAAAGCGGTAGATTACC 26
                                                                                                                                                                                                                                                                                 Example 1; Fig 1; 67pp; English
                                                                                                                          (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS08432 standard; DNA; 66 BP.
                                                                                             21-JAN-2000; 2000US-0177437
                                                                   19-JAN-2001; 2001WO-US02024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-2001 (first entry)
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Matches 26, Conservative
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/label= '
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                                                                                                                                                                               WPI; 2001-476118/51
                                                                                                                                                       Bruce WB, Niu X;
            W0200153476-A2.
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                                         26-JUL-2001
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                                                                                                                                                                                                                                                       herbicides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPES are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. absorbs stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fundi, bacteria,
                                                                                                                                                                                                 Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Root-preferred promoter element: RPE; abiotic stress: drought; salinity; pesticide resistance: biotic stress: disease resistance; tungal disease; bacterial disease; viral disease; insert affack; nematode attack; RPEB; random oliqonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.4%; Score 24; DR 22; Length 66; 100.0%; Pred. No. 0.0017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A plant root-preferred promoter element (RPE), RPE 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 66 BP; 19 A; 12 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "5'_flanking_sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 ATTACCGTCCTACGAATTCAGGTG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 ATTACCGTCCTACGAATTCAGCTG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viruses, insects and nematodes).
                                                                                       (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                         Claim 5; Fiq 1; 45pp; English.
                 19-JAN-2001; 2001WO-US02011.
                                                  21-JAN-2000; 2000US-0177473.
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/*t.ag=
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                                                                                                                                                              WPI: 2001 442261/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                             Bruce WE, Niu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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The sequence represents a plant root preferred promoter element, RPE, isolated from a random oligonucleotide library (Rol). The invention concerns a method of identifying and isolating tissue preferred promoter elements comprising the use of a mixture of random oligonacteotides,
                                                                                                                                                                                                                                               Producing Lissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating Lissue-preferred promoter elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPEs are useful in the genetic manipulation of a plant when operably
linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                                                                                                                                          flanked by 5' and 3' flanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue-specific promoters from plants, including but not limited to
root-specific promoters or root-preferred promoter elements (RPE). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Root-preferred promoter element; RPE; abiotic stress; drought; salinity; pesticide resistance; horbicide resistance; biotic stress; disease resistance; tungal disease; barterial disease; viral disease; insert attack; nematode altack; RPE/3; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by lundi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24; DB 22; Length 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A plant root-preferred promoter element (RPE), RPE 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 66 BP; 20 A; 12 C; 21 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.0017;
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"5'_flankind_sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viruses, insects and nematodes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 ATTACCGTCCTACGAATTCAGCTG 66
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                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1; 45pp; English.
                                                                                                                                          (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS08447 standard; DNA; 66 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                      21-JAN-2000; 2000US-0177473.
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                                                                    19-JAN-2001; 2001WO-US02011
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Best Local Similarity
MO200153502-A2
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                                                                                                                                                                              Bruce WB,
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49..66

misc_feature

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The sequence represents a plant root-preferred promoter clement, RPE, isolated from a random oligonocleotide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonocleotides, flanked by 5 and 3' flanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCE amplifying the bound oligonocleotide. The method is used for isolating tissue specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE). The RPEs are useful in the genetic manipulation of a plant when operably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                                                             Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Root-preferred promoter element, RPE; abiotic stress; drought, salinity; pesticide resistance; horbicide resistance; biotic stress; disease resistance; fungal disease; bacterial disease; viral disease; insect attack; nematode attack; RPES9; random oligonucleotide library;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.4%; Score 24; DB 22; Length 56; 100.0%; Pred. No. 0.0017; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A plant root-preferred promoter element (RPE), RPE 89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 66 BP; 19 A; 11 C; 21 G; 15 T; 0 other;
 /*tag- c
/label= "3'_flanking_sequence"
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/label= "5'_flanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viruses, insects and nematodes),
                                                                                                                                                                                                                                                                                                                                                                                       Example 1: Fig 1: 45pp; English
                                                                                                                                                                                                    (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                             19-JAN-2001; 2001WO-US02011.
                                                                                                                                                                21-JAN-2000; 2000US-0177473.
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Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19..48
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                                                                                                                                                                                                                                                                            WPI; 2001-442261/47.
                                                                                                                                                                                                                                          Bruce WB, Niu X;
                                                     W0200153502-A2
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                                                                                           26-JUL-2001
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The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonuclectide library (RCL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonuclectides, flanked by 5' and 3' flanking sequences, which hybridise to tissuespecific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating tissue-specific promoters from plants, including but not limited to troot-specific promoters or root-preferred promoter elements (RPE). The RPES are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                                                                                Producing tissue-preferred promoter elements constructs for regularing expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fungi, bacteria,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A plant root.preferred promoter element (RPE), RPE 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 66 BP; 19 A; 11 C; 21 G; 14 T; 1 other.
                                                                        "3'_flankinq_sequence"
               /note= "Randomised sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       viruses, insects and nematodes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 ATTACCGTCCTACGAATTCAGCTG 66
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                                                                                                                                                                                                                                                          PION-) PIONEER HI-BRED INT INC
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les 24; Conserv
                                                                                                                                                                                                                                                                                             Bruce WB, Niu X;
                                                                                                        WO200153502-A2
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPES are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                                                                                                                                    Producing Lissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating Lissue-preferred promoter elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koot-preferred promoter element; RPB; abiotic stress; drought; salinity; pesticide resistance; herbicide resistance; biotic stress; disease resistance; fundal disease; bacterial disease; viral disease; insect attack; nematode attack; RPB73; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fundi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a plant root-preferred promoter element, RPE,
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Pred. No. 0.0017;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 66 8P; 20 A; 12 C; 20 G; 13 T; 1 other;
a
"5' flanking_sequence"
                                                                                                          c
"3'_flanking_sequence"
                                                                   /note- "Randomised sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viruses, insects and nematodes).
                                                                                                                                                                                                                                                                                                             (PION-) PIONEER HI-BRED INT INC.
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19..48
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 /*tage
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Matches 24; Conserv
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                                                                                                                                                                                                   26-JUL-2001
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isolated from a random oligonucled(ide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred premoter elements comprising the use of a mixture of random oligonucledides, tlanked by 5' and 3' flanking sequences, which upbridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue-specific promoters from plants, including but not limited to rook-specific promoters or root-preferred promoter elements (RHE). The RPFs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, posticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fundi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Root-preferred promoter element, RPE, abiotic stress; drought, salhnity, posticular ersistance, herbicide resistance, biotic stress; disease resistance; fundal disease, bacterial disease, viral disease; insect attack; nematode attack; RPES; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents a plant root-preferred promoter element, MPE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 66 BP; 19 A; 12 C; 22 G; 14 T; 0 other;
                                                                                                                                                                     "3'_flanking_sequence"
                                                               "5'_tlanking_sequence"
                                                                                                 b
"Randomised sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
             Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viruses, insects and nematodes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 1; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                              (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                           19-JAN-2001; 2001WO-US02011.
                                                                                                                                                                                                                                                                                                            21-JAN-2000; 2000US-0177473.
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                                                                                                 /*tag-
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                                                                                  19..48
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Matches 22; Conserve
                                                                                                                                                                                                                                                                                                                                                                                  Niu X
                                                                                                                                                                                                         WO200153502-A2
                               misc feature
                                                                                    misc_feature
                                                                                                                                       misc_feature
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Synthetic.

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100.0%;
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Matches 19; Conservative
                                                                                       1..18
/*tag=
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                                                                                        misc_feature
                                                                                                                            misc feature
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                                                         Synthetic.
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                                    SS
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                                                                                                                                                                                                                                                                                                                                                                                                          isolated from a random oligonuclectide library (ROI). The Invention Concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonuclectides, flanked by 5' and 3' flanking sequences, which hybridise to tissue specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonuclectide. The method is used for isolating tissue-specific promoters from plants, including but not limited to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       root-specific promoters or root-preferred promoter elements (RPE). The RPES are useful in the genetic manipulation of a plant when operably allohed to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fungi, bacteria, viruses, insects and nematodes).
                                                                                                                                                                                                                                                                                                                            Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements
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                                                                                                                                                                                                                                                                                                                                                                                                 the sequence represents a plant root-preferred promoter element, RPE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Root-preferred promoter element; RPE; abiotic stress; drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.3%; Score 20; DB 22; Length 65; 100.0%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A plant root-preferred promoter element (RPE), RPE 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 65 BP; 18 A; 14 C; 17 G; 16 T; 0 other;
                                                                 /*tag= a
/label= "5'_flanking_sequence"
                                                                                                                                   /*tag- c
/label= "3'_flanking_sequence"
                                                                                                 b
"Randomised sequence"
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                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pr
                                                                                                                                                                                                                                                             (PION-) PIONEER HI-BRED INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS08437 standard; DNA; 62 BP
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                                                                                                              /note=
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                                                                                                                        48..65
                                                      1..18
                                                                                                                                                                                                                                                                                                         WPI; 2001-442261/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                   WO200153502-A2.
                                                     misc_teature
                                                                                                                         misc_feature
                                                                                      misc_feature
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                                                                                                                                                                                           26-JUL-2001
                     Synthetic.
                                                                                                                                                                                                                                                                                   Bruce WB,
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ROL; SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing Lissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating Lissue-preferred promoter elements
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salinity; pesticide resistance; horbicide resistance; biotic stress; disease resistance; fungal disease; bacterial disease; viral disease; insect attack; nematode attack; RPE2; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saps
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Pred. No. 0.85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "3'_flanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                                a
"5′_1lanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     b
"Randomised sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PION-) PIONEER HI-BRED INT INC.
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(first entry)

26-SEP-2001

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The sequence represents a plant root-preterred promoter element, RPE, isolated from a random oligonuclectide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, flamked by 5° and 3′ flamking sequences, which hybridise to tissue specific plant nuclear proteins, isolating the complexes and PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing ilssue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amplifying the bound oligonucleotide. The method is used for isolating
tissue-specific promoters from plants, including but not limited to
root-specific promoters or root-preferred promoter elements (RPE). The
                               Root-preferred promoter element, RPB, abiotic stress, drought, salinity; pesticide resistance, herbicide resistance; biotic stress, disease resistance; fungal disease; bacterial disease; viral disease; inseet attack; nemalode attack; RPE22; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPEs are useful in the genetic manipulation of a plant when operably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stress (disease resistance, resistance to attack by fungi, bacteria,
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0
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plant root-preferred promoter element (RPE), RPE 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 66 BP; 19 A; 11 C; 21 G; 15 T; 0 other;
                                                                                                                                                                                                         a
"5'_tlanking_sequence"
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Pred. No. 0.84;
                                                                                                                                                                                                                                                                       /note= "Randomised sequence"
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                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.55,
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viruses, insects and nematodes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-2001; 2001WO-US02011.
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                                                                                                                                                                                                                                                                                            49..66
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                                                                                                                                                                                                                                                                                                                                                          WO200153502-A2
                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                          misc_teature
                                                                                                                                                                                                                                                                                            misc_teature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bruce WB,
                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                       ROL; SS.
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The sequence represents a PCR primer which binds to the 5' flanking region of a random oligonucleotide library (RGL) construct used to isolate tissue-specific promoter elements. The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, flanked by 5' and 3' tlanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating tissue-specific promoters from plants, including but not limited to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPEs are useful in the genetic manipulation of a plant when operably
linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           achieve a desired phenotypic effect, e.g. abiotic stress (drought, treperature, salinity, pesticide and horbicide resistance) and blotic stress (disease resistance, resistance to attack by fundi, bactoria, viruses, insects and nematodes).
                                                                               Root-preferred promoter element, RPE, abiotic stress; drought; salinity; pesticide resistance; horbicide resistance; biotic stress; desease resistance; fungal disease; bacterial disease; viral disease; instack; nematode attack; random oligonucleotide library; ROE; n19808; ss; PCK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Root-preferred promoter element: RPE; abiotic stress; drought; salinity; pesticide resistance; herbicide resistance; biotic stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          root-specific promoters or root-preferred promoter elements (RPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 22; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A random oligonucleotide library, ROL, PCR primer n19811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                  A random oligonucleotide library, ROL, PCR primer n19808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 21; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS08442 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                   19-JAN-2001; 2001WO-US02011;
                                                                                                                                                                                                                                                                                                                                                       21-JAN-2000; 2000US-0177473,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGAGATCTGGATGCGTTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-442261/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                26-JUL-2001.
                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bruce WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS08442;
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AAS08441 standard; DNA; 18 BP

RESULT 14 AAS0844] AAS08441;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissue-specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE). The RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and horbicide resistance) and bictic
                                                                                                                                                                                                                                                                                                                                                                         Producing Lissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating Lissue-preferred promoter elements
disease resistance, fungal disease, bacterial disease, viral disease, insect attack; nematode attack; random oligonucleotide library; ROL; n19811; ss; PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               salinity; pesticide resistance; herbicide resistance; biotic stress; disease resistance; fungal disease; bacterial disease; viral disease; insect attack; nematode attack; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stress (disease resistance, resistance to attack by fundi, barteria, viruses, insects and nematodes).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.3%; Score 18; DB 22; Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 21; 45pp; English
                                                                                                                                                                                                                                                                (PION-) PIONEER HI-BRED INT INC.
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                                                                                                                                                                                                                          21-JAN-2000; 2000US-0177473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 GTCCTACGAATICAGCTG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 GTCCTACGAATTCAGCTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442261/47.
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                                                                                                             WO200153502-A2.
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                                                                            Synthetic
                                                                                                                                                                                                                                                                                                    Bruce WB,
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AAS08443/c
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The sequence represents a PCR primer which binds to the 3' flanking readion of a random oligonucleotide library (ROL) constructused to isolate Lissue-specific promoter elements. The invention concerns a method olidentlying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, flanked by 5' and 3' flanking sequences, which hybridise to tissuespecific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating tissue-specific promoters from plants, including but not limited to reopt-specific promoters or root-preferred promoter clements (RPE). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements
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linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A random oligonucleotide library, ROL, PCR primer n19810.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 23; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viruses, insects and nematodes).
                                                                                                                                                                                                                                                             (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                    21-JAN-2000; 2000US-0177473
                                                                                                            19-JAN-2001; 2001WO-US02011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 TGAGATCTGGATCCGTTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              WPI: 2001-442261/47
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200153502-A2.
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                                        26-JUL-2001
                                                                                                                                                                                                                                                                                                                                 Bruce WB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS08444
REAL PROPERTY OF THE PROPERTY 
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                                                                                                                                                               region of a random oligonucleotide library (ROL) construct used to isolate tissue-specific promoter elements. The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, tlanked by 5' and 3' flanking sequences, which hybridise to Lissue-specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating
                                                                                                                                                                                                                                                                    root-specific promoters or root-preferred promoter elements (RPE). The RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
                                                                         Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Root-preferred promoter element, RPE; abiotic stress; drought; stress; posticide resistance; brobloide resistance; biotic stress; dispase resistance; fungal disease; bacterial disease; viral disease; insect attack; nematode attack; RPE29; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                      achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                        tissue-specific promoters from plants, including but not limited to
                                                                                                                                                    the sequence represents a PCR primer which binds to the 5' flanking
                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 22; Length 18; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A plant root-preferred promoter element (RPE), RPE 29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "5'_tlanking_sequence"
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/note= "Randomised sequence"
                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                             Sxample 1; Page 23; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      27.3%; Scur.
100.0%; Pre-
0; ?
                                                                                                                                                                                                                                                                                                                                                 viruses, insects and nematodes).
(PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTCCTACGAATTCAGCTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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/*tag-
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                                                 WPI; 2001-442261/47
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es 18; Conserv
                          Niu X;
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                          Bruce WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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The sequence represents a plant root-preferred promoter element, RFE, isolated from a random oligonureledide library (RGL). The invention concerns a method of identifying and isolating tissue-preferred promote elements comprising the use of a mixture of random oligonucleotides, flanked by S, and S, Tlanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonurleotide. The method is used for isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (MPE). The RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                    Producing Lissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     achieve a desired phenotypic effect, e.g. abiolic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fundi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Root-preferred promoter element, RPE; abiotic stress; drought; salinity, pesticide resistance; herbicide resistance; brotal disease resistance; fungal disease, barterial disease; viral disease; insect attack; nematode attack; RPE61; random oligonnelectide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A plant root-preferred promoter element (RPE), RPE 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 64 BP; 16 A; 13 C; 17 G; 18 T; 0 other;
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"5'_tlanking_sequence"
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/label= "3/_flanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                      isolating tissue-preferred promoter elements -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.9;
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"Randomised sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viruses, insects and nematodes).
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                                                                                                                      (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Flg 1; 45pp; English.
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19-JAN-2001; 2001WO-US02011.
                                                           21-JAN-2000; 2000US-0177473.
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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                                                                                                                                                                                    Bruce WB,
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Bruce WB, Niu X;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                      The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonuclecticd library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides.
                                                                                                                                                  Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements -
                                                                                                                                                                                                                                                                                                    tissue-specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE). The RPES are useful in the generic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                   flanked by 5' and 3' flanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Root-preferred promoter element, RPE, abiotic stress, drought, salinity, pesticide resistance, herbicide resistance, blotic stress; disease resistance, fundal disease, bacterial disease, viral disease, insect attack; nematode attack; RPE60, random oligonucleotide library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 22; Length 64; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A plant root-preterred promoter element (RPE), RPE 60.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 64 BP; 22 A; 11 C; 16 G; 15 T; 0 other;
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"Randomised sequence"
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                                                                                                                                                                                                                                                                                                                                                                                      viruses, insects and nematodes).
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                                                                               (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                               Claim 5; Fig 1; 45pp; English.
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                                  19-JAN-2001; 2001WO-US02011
                                                        21-JAN-2000; 2000US-0177473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGAGATCTGGATCCGTTC 18
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19..47
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                                                                                                                            WPI; 2001-442261/47
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nes 18; Conserv
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            26-JUL-2001.
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                                                                                                       Bruce WB.
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The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonuclectide library (RUL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonuclectides, flanked by 5' and 3' flanking sequences, which hybridise to tissuespecific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonuclectide. The method is used for isolating tissue-specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE). The RPEs are useful in the genefic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     achieve a desirred phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, posticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by lungi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 2.9;
0; Mismatches 0; Indels
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/label= "5'_flanking_sequence"
19..47
/label= "3'_flanking_sequence"
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                                                                                                                                                                                                                                                                                                           21-JAN-2000; 2000US-0177473.
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Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                             isolated from a random oligonucleotide library (RGL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, flanked by 5' and 3' flanking sequences, which hybridise to tissuespecific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating
                                                                                                                                                                                                                                                                                                                                                                                                      tissue-specific promoters from plants, including but not limited to root specific promoters or root-preferred promoter elements (RRE). The REPS are useful in the generic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. abiotic stress (drough, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                        Producing Lissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identitying and isolating Lissue-preferred promoter elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koor preferred promoter element, RPE, abiotic stress, drought, salinity, pesticide resistance, herbicide resistance, biotic stress, disease resistance, fingal disease, bacterial disease, viral disease, insect attack; nematode attack; random oligonucleotide library.
                                                                                                                                                                                                                                                                                                                   The sequence represents a plant root-preferred promoter element, RPE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%; Score 18; DB 22; Length 65; 100.0%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A random oligonucleotide library, RoL, sequence n19813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Séquence 65 BP; 19 A; 13 C; 18 G; 15 T; 0 other;
                                     /label= "3' flanking sequence"
/note= "Randomised sequence"
48..65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             viruses, insects and nematodes).
                                                                                                                                                                (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                                          Claim 5; Fiq 1; 45pp; English.
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                                                                                                              19-JAN-2001; 2001WO-US02011.
                                                                                                                                        21 JAN - 2000; 2000US - 0177474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGAGATCTGGATCCGTTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGAGATCTGGATCCGTTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
                        /*t.ag-
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/*tag-
                                                                                                                                                                                                                  WPI; 2001-442261/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n19813; ss.
                                                              WO200153502-A2
             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                       26 - JUL - 2001
                                                                                                                                                                                         Bruce WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS08440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS08440
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used to isolate tissue-specific promoter elements. The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oliquouelectides, flanked by 5' and 3' flanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCK amplifying the bound oliquouelectide. The method is used for isolating tissue-specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a random oligonucleotide library (RoL) construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPEs are useful in the genetic manipulation of a plant when operably
linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Root-preferred promoter element, RPE, abiotic stress, drought; salinity, pesticide resistance; horbicide resistance; biotic stress, disease resistance; tungal disease, bacterial disease, viral disease, instance, remained attack; RPE71; random oligenucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            achieve a degired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fundi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                             c
"3'_1lanking_sequence"
/label= "5'_tlanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66 BP; 7 A; 9 C; 9 G; 11 T; 30 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolating tissue-preferred promoter elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.9;
                                                                                            "Randomised sequence"
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 21; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viruses, inserts and nematodes).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                                                                                                                                    19-JAN-2001; 2001WO-US02011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                             /*t.aq=/
/label
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/*tag=
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                                                                                                                                                                                                                                                         WO200153502-A2.
                                  misc_feature
                                                                                                                              misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bruce WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Logal :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue-specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE). The RPES are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic ellect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated from a random oligonucleotide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, tlanked by 5 and 3′ flanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR amplifying the benefit of the complexes and PCR amplifying the benefit of the complexes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying an isolating tissue-preferred promoter elements -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                        AAS53852 standard; DNA; 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000;
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             Helicobacter pylori
                                               antibiotic;
                                                                                           Helicobacter pylori DNA for cellular proliferation protein #306
                                                                                                                                                           AAS53852
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 66
                                                                                                                                                                                                                                                                                                                                                                                                                               viruses, insects and nematodes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amplifying the bound oligonucleotide. The method is used
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                                             Antisense; ds: prokaryotic cellular proliferation gene antibiotic; antibacterial; drug design.
                                                                                                                           13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                              stress (disease resistance, resistance to attack by fungi, bacteria,
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                                                                                                                                                                                                                                                                      2 GAGATCTGGATCCGTTCG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a plant root-preferred promoter element, lated from a random oligonucleotide library (ROL). The invent
                                                                                                                                                                                                                                                                                                   GAGATOTGCATOCGTTCG 19
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                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                          (first entry)
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19..48
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                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "5'_flanking_sequence"
                                                                                                                                                                                        BP
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                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                 Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                   NO.
                                                                                                                                                                                                                                                                                                                                                   2,9;
                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                              Length 66
                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                  0,
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ID AAF608
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23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electron format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      programmes. The antisense nucleic acid sequence is also useful to scree
for homologous nucleic acids which are required for cell proliferation
a wide variety of organisms. The present sequence encodes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to antisense inhibitors of genes essential to prokaryotic collular proliferation, their use in identifying the genes, their use in the discovery of novel antiblotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; Seq ID No 7489; 511pp; English
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23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200170955-A2
               Pseudomonas
                                            plant development; plant yield;
                                                           Export system;
                                                                                        Pseudomonas sp export system associated DNA ORF11349a
                                                                                                                                                        AAF60852;
                                                                                                                                                                                       AAF60852 standard; DNA; 1168 BP
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                          16-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention is also useful for the identification of potential new targets
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELII-) ELITRA PHARM
                                                                                                                                                                                                                                                                   192 TAAAAAAGCGGTAGAT
                                                                                                                                                                                                                                                                                                 29 TAAAAAAGCGGTAGAT 44
                                                                                                                                                                                                                                                                                                                                Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
Pseudomonas aeruginosa and Enterococcus faecalis. The
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                ВP;
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2000US-242578P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen
                                          transgenic plant; translocation; plant growth; ent; plant yield; soil quality; phytoprotection;
                                                                                                                                                                                                                                                                                                                                                                                               142 A; 78 C; 125 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                   207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The antisense nucleic acids can also be used
                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                Score 16;
                                                                                                                                                                                                                                                                                                                                               Pred.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1) for expression of recombinant export systems; (2) as probes and primers for detection, isolation and amplification of full-length cDNA sequences; and (3) for producing transpenic plants. Cells transformed with (1), also recombinant export systems or synthetic peptides or proteins with the same activities, are used to promote growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the vector of (a); (c) production of export systems by culturing cells (b); (d) (partial) expression products (II) of (I), and synthetic proteins or peptides with the same sequences; (e) mono- or poly-clonal antibodies (Ab) specific for (II); (f) hybridoma cells that produce monocional Ab; and (q) transgunic plants that contain cells of (b). The export systems encoded by (I) transiocate, through the bacterial cell wall, endogenous or modified metabolities or endogenously or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GBFB )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE19935105-A1
                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 10673
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1168 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             describes (a) recombinant expression vectors containing (1): (b) prokaryotic and eukaryotic cells transformed or transfected with (1) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
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  23-MAR-2001;
                            27 - SEP - 2001
                                                     W0200171042-A2
                                                                              brosophila melanogaster
                                                                                                      pharmaceutical; gene; ss
                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide
                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                 VIETO2332
                                                                                                                                                                                                                         ABL05397 standard; cDNA; 2731 BP
                                                                                                                                                                                                                                                                                                                                                                                                                              development and yield of plants, particularly Leguminosae. Host cells that express export systems improve soil quality, are phytoprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim Ba; Page 24-25; 26pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heterologously expressed proteins. (I), and their fragments, are useful:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     having the biological function of export systems. The invention also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel DNA sequences (1) that express products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER
                                                                                                                                                                                                                                                                                                                                                                                                                   improve development, growth and yield of plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding a bacterial export system, useful for promoting growth
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GES BIOTECHNOLOGISCHE FORSCHONG MBH
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 2001WO-US09231.
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Matches 16; Conserv
Claim 8; Page 1580-1581; 2188pp; English
                                                                                                                                                                      09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                          03-SEP-2001
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11-JUL-2000; 2000US-0614150.
                                                                WP1; 2001-316495/33.
                                                                                         Kimmerly
                                                                                                                                             :6661-AON-60
                                                                                                                                                                                                 17-MAY-2001
                                                                                                                                                                                                                         WO200134809-A2
                                                                                                                                                                                                                                                 Staphylococcus epidermidis
                                                                                                                                                                                                                                                                        vaccination; endocarditis;
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                                                                                                                                                                                                                                                                                                                                                                  AAH54560;
                                                                                                                  (GLAX ) GLAXO GROUP LID
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discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded profeins (ABB57737-ABB72072).
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Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -

    epidermidis genomic polynucleotide sequence SEQ ID No:3924

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Best Local o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH52304 to AAH53970 represent nucleic acids (1) encoding polypeptides (11), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (1) and (11) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (1) may be used to produce the secondary of them which are used to production of vectors containing them which are used to produce hosts coils which express the polypeptides. The polypeptides (11) (and/or nucleic acids) may then be polypeptides. The polypeptides (11) (and/or nucleic acids) may then be
AAH52304 to AAH53970 represent nucleic acids (1) encoding polypeptides (II), given in AAGB1454 to AAGB3120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are in the exemplification of the present invention.
                                                                                                                                                                          Nucleic acids encoding polypeptides from Staphylococcus epidermidis useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200134809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis SR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. epidermidis genomic polynucleotide sequence SEQ ID NO:3336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SFQ ID NO:4465 to 4472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to vaccinate subjects and to raise antibodies against the bacteria
                                                                                                                                       Claim 8; Page 881-882;
                                                                                                                                                                                                                                                                                                              (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                     09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH53972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endocarditis;
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                                                                                                                                                                                                                                                                                                                                                 99US-0164258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     939 A; 600 C; 422 G; 1071 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.2%;
100.0%;
                                                                                                                                     2188pp; English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain; infection; diagnosis
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Best Local
                                                                                                      (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the s. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodics against the bacteria used to vaccinate subjects and to raise antibodics against the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides. The polypeptides (ii) (and/or nucleic acids) may then be used to vaccinate subjects and to raise anthodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA
AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
                                         The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis SRI strain; vaccination; endocarditis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3246 BP; 1091 A; 533 C; 536 G; 1086 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472
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N.B. The present invention specifically claims all the polynucleotide
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                                                                                                                                                                                                                                                                                                      Claim 8;
                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides from Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-316495/33
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                                                                                                                                                                                                                                                          AAH52304 to AAH53970 represent nucleic acids (1) encoding polypeptides
                                                                                                                                                                                                                                                                                                                                             useful for vaccinating against infections, e.g. endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CLAX ) GLAXO GROUP LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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                                                                                                                                                                                                                                                                                                 Page 1923-1925; 2188pp; English.
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100.0%;
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Pred. No.
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RESULT: 40
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N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                        sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                              useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster expressed polynucleotide SEQ ID NO 10670
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                                                                                                                 Sequence 7345 BP;
                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 10670; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid
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11 JUL 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4019 BP; 1292 A; 738 C; 623 G; 1366 T; 0 other;
                                                                                                                                                                    at ttp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                             capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 MAR-2002
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Conservative (
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2000US-0614150
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                                                                                                              1957 A; 1658 C; 1667 G; 2063 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.2%;
                                                           24.2%; Score 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection reagent for detecting 1000 or more
for elucidating cell signalling and cell-cell
     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
        Mismatches
                                   N
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO.
                                                           DH 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4019;
                                                        Length 7345;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>..</u>
     0;
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  Gaps
                                                                                                                                                                                                     Odim
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RESULT 32
AAQ24203/c
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ID AAF222
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                                                                                                                                                                                                                                                      RESULT 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                  Best Local
                                                                                                                                                        63894 ATCCGTTCGACAAAAC 63879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
BTG; acyl rearrangement; deamination; PCR; signal; ss
                                                                                                                                                                                                                                                                                      the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clott
                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6026 GACAAAACGGTAAAAA 6011
                       Transglutaminase Primer 4.
                                              09-0CT-1992
                                                                                            AAQ24203 standard; DNA;
                                                                                                                                                                                                                                                    Sequence 86584 BP;
                                                                                                                                                                                                                                                                             factors,
                                                                                                                                                                                                                                                                                                                                                             Claim 102; Page 607-626; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WP1: 2000-587529/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prouss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200055325-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centromere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF22292:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF22292 standard; DNA; 86584
                                                                                                                                                                                                                                                                                                                producing stably inherited michrosomes which can serve as vectors for
                                                                                                                                                                                                                                                                                                                         The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thatiana) centromere. The constructs are usoful for
                                                                                                                                                                                11 AFCCGTTCGACAAAAC
                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 GACAAAACGGTAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  containing repeats from centromeres 1-4 #15
                                                                                                                                                                                                                                                                                                                                                                                                                                                           D, Copenhaver
                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                             cytokines, antibodies, and growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            michrosome;
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US07392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0125219.
99US-0127409.
99US-0134770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0153584
99US-0154603
                                                                                                                                                                                                                                                       26755 A;
                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                               24.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ċ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ن<u>ي</u>
4
                                                                                               36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keith
                                                                                                                                                                                                                  Score 16; DB 21; pred. No. 18;
                                                                                                                                                                                                                                                      16841 C; 17276 G;
                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dЯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>..</u>
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                          interleukins, clotting
                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                    25711 T; I other
                                                                                                                                                                                                                               Length 86584;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                         0;
                                                                                                                                                                                                         Gaps
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RESULT 33
AADO3192/c
ID AADO31
AC AADO31
XX AADO31
XX COYD;
KW COYD;
KW GOVETO
KW GENVITO
KW GENVITO
KW GENVITO
KW GENOLD
KW GENVITO
KW GENOLD
KW 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 15
                                                                                                                                                                               form, 700266438 clone: promoter: morphology: physiology: growth; seed: development; nutritional enhancement; discase resistance; plant embryo: environmental tolerance; chemical tolerance; pest resistance; qenetic environmental tolerance; chemical tolerance; pest resistance; quenetic environmental tolerance; pest primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to Glu residues by deamination. The enzyme is used in the product of gelled loods, gelled cosmetic yoqurt, gelatin, cheese etc. It is also used in the product of thermally stable materials such as microcapsules and carriers of immobilized enzymes. The DNA sequence given allows the product HTG efficiently and in large quantity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qp. of glutamine. It introduces intra- or intermolecular formation
of epsilon (gamma-Gln)-Lys cross-linking when an epsilon-amino gp.
of a Lys residue acts as an acyl receptor. When water acts as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        given in AAQ24202 to amplify a portion of the BTG gene using PCR techniques. The portion of the gene amplified contained the signal, pro and structural sequences from BTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                     PCR primer #2 used to isolate Zea mays 700266438 clone promoter cDNA
                                                                                                                                                                                                                                                                                                                                    13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 27; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA tragment encoding trans:qlutaminase - is in vector, e.g. PnJ1053-BTG, for protein expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-001-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP481504-A
                    30-AUG-2000; 2000WO-US23824
                                                                08-MAR-2001
                                                                                                        MO200116307-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    AAD03192 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acyl acceptor the enzyme accelerates the conversion of Gln residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This DNA sequence was used in conjunction with the primer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-133808/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AJIN ) AJINOMOTO CO INC
(AMAN ) AMANO PHARM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-001-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IGAGATOTGGAICCG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catalyses an acyl rearrangement reaction of a gamma-carboxyamide
                                                                                                                                                mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAGATCTGGATCCG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arafuka S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90JP-0282566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91EP-0117813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koikeda S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 C; 7 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.7%; Score 15; DB 13; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                      44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsui H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is inserted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 34
AAN60630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XX AX XX B
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                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                            misc_RNA
                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enhancement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-1999;
  02-JUL-1985;
                                          09-JAN-1986
                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN60630
                                                                                  DE3523634-A
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Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         also useful for expression of transgene products in plant embryos and plant seeds. The plant promoters are useful for modifying plants through genetic engineering to have the desired characteristics associated with plant morphology, physiology, growth and development yield, nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to nucleic acid sequences for regulating gene expression in plants. The promoter nucleic acid molecules are useful for controlling gene expression in plants. The promoter DNA sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New plant regulatory DNA sequences, useful for selectively controlling gene expression and for modifying plants through genetic engineering to have the desired morphology, physiology, growth or nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-urogastrone - beta-lactamase fusion gene from pUG2301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN60630 standard; DNA; 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 44 BP; 9 A; 18 C; 6 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 72; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-244405/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-urogastrone gene; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enhancement, diseases or pest resistance, or environmental or chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                        tusion protein; beta-lactamase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 700266438 glone promoter cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a PCR primer used along with an adaptor primer (AP2) (AAD03171) in the nested PCR reaction to isolate Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RENE-) RENESSEN LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGAGATCTGGATCCG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAGATCTGGATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0151892
                                                                                                                                                                                                                             /product-
1..188
                                                    /label= adaptor
199..357
                                                                                                                                          /product= beta-lactamase
189..198
/product- beta-urogastrone
                              /*tag=
                                                                                                           /*tag=
                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                     /*tag−
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.7%; Score 15;
                                                                                                                                                                                                     c
                                                                                                                                                                                                                                                                                     D
                                                                                                                                                                                                                                                      fusion_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        salivary gland; ulcers; wounds ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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85DE-3523634

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RESHLT 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protects beta-urogastrone and beta-lactamase collects in the periplasm of E.coli. It is therefore easy to collect and purify the product.

Nota-urogastrone is the hormone of the salivary glands which supresses stomach acid secretion and promotes cell growth, so is useful for treating ulcers and wounds. Previously the product was obtd. only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   easily recovered from the fusion protein expressed by transformants. The fusion protein is less easily degraded by proteases and so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drid
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                          Identification of regulatory regions modulated by a cellular insult,
                                                                                                                                                                                                                                                       23 OCT-1996;
                                                                                                                                                                                                                                                                                                            24-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                        US6025141-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stress responsive regulatory region; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E.coli promoter region flanking sequence, DPD2087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 MAY - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ91620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ91620 standard; DNA; 533 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 478 BP; 111 A; 102 C; 125 G; 140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene and insertion into plasmids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 55-56; 92pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsushiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EART-)
                                                                                                                                                                                                                                                                                                                                                                15-FEH-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    luxCDABE gene complex; crop protection chemical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence includes the sequence of claim 1 (bases 199-357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ACATCTGGATCCGTT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene for expression of beta-urogastrone transformed cells contg. it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          small amts, from human urine, also AAN60628, and 30-32.
                                                                                     2000-181802/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAITCTGGATCCGTT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1986-015031/03
                                                                                                                                             ₹>,
                                                                                                                                                                                                  DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARTH CHEMICAL COL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP60626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region; regulatory region identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insult, luciterase; thermostable lux gene complex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by restriction sites for coupling to the beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                       Van Dyk TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ξ
                                                                                                                                                                                                                                                    9608-0735545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15;
                                                                                                                                                                                                  COE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hiramatsu H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-urogastrone can then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DH 7; Length 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koumoto S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              upper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derivs., plasmid(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         flanking sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caps
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such as crop protection chemicals

are useful for detecting crop protection chemicals and for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
The specification describes an Escherichia coli regulatory region modulated by a cellular insult. The regulatory region is preferably sultometuron methyl (SM) responsive regulatory region, preferably bound by the sequences given in AAF55139-40. The recombinant E. coli
                                                                                                   Claim 13; Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli; regulatory region; cellular insult: crop protection; sulfometuron methyl-responsive regulatory region; cellular stress; herbicide; environmental pollutant; heavy metal; oxidative damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modulated by the cellular insult. The method is useful for identifying regulatory regions affected by cellular stress such as that created by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phase with a cellular insult; and (d) analysing the fusion-containing strain for a change in luminoscence, the change in luminoscence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modulated by a cellular insult, comprising: (a) creating a library of gene fusions of genomic DNA fused to a promoterless, luminescent reporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is a tlanking sequence for an E. coli promoter region. The invention relates to a method for identifying regulatory regions
                                                                                                                                           consists of sulfometuron methyl-responsive regulatory region
                                                                                                                                                                regulatory elements responsive to variety of cellular stresses,
                                                                                                                                                                                  Novel Escherichia coli genomic segment, useful for detecting bacterial
                                                                                                                                                                                                                           WPI: 2001-217925/22.
                                                                                                                                                                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO E
                                                                                                                                                                                                                                                                                                                                              23-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                     24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                            27 - FEB - 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6194159-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anaerobiosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sulfometuron methyl-responsive regulatory region binding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF55139 standard; DNA; 533 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 533 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          responsive regulatory regions undetectable by prior art methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erop protection chemicals. The method can detect promoters or stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          indicating that the fusion-containing strain includes a regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (b) culturing individual gene fusion-containing strains in liquid media;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complex in Enteric bacteria to create fusion-containing strains;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Renella species, a thermostable lux gene complex, and a luxCDABE gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Column 29-30; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (c) contacting the fusion containing strains at a particular growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complex selected from a gene complex encoding luciferase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
15; Conser
                                                                                                                                                                                                                                                                  æΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                              96US-0735545
                                                                                                                                                                                                                                                                                                                                                                                     99US-0449083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 A; 94 C; 140 G; 133 T; 0 other;
                                                                                                   29-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.78;
                                                                                                 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15;
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 37
ANABOB 32
ANABOB 32
ANABOB 32
ANABOB 32
ANABOB 33
ANABOB 32
ANABOB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacterial regulatory elements responsive to a variety of cellular stresses (produced by cellular insults) such as herbicides, environmental pollutants, heavy metals, changes in temperature, changes in pH, agents producing oxidative damage, insults causing DNA damage, insults causing anaerobiosis, and biological insults such as the
                                             This sequence includes the sequence of claim 1 (bases 319-477) modified by restriction sites for coupling to the beta-lactamase gene and insertion into plasmids. Beta-urogastrone can then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-uroqastrone gene; hormone;
tusion protein; beta-lactamase;
                                                                                                                                            Disclosure; Page 59-61; 92pp; German.
                                                                                                                                                                                                                                                                                                                                           Matsushiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                           02 · JUL - 1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JAN-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE3523634-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN60632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN60632 standard; DNA; 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 533 BP; 166 A; 94 C;
                                                                                                                                                                                                                                                                      F-PSDB;
                                                                                                                                                                                                                                                                                                                                                                  Aoki S.
                                                                                                                                                                                                                                                                                                                                                                                                                (EART-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogenic life forms.
                         easily recovered from the fusion protein expressed by transformants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 ANANCGGTAAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 AAAACGGTAAAAAAG
fusion protein is less easily degraded by proteases and
                                                                                                                                                                                            transformed cells contg. it.
                                                                                                                                                                                                                      gene for expression of beta-urogastrone
                                                                                                                                                                                                                                                                   1986-015031/03.
DB; AAP60628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                             EARTH CHEMICAL COL
                                                                                                                                                                                                                                                                                                                                                               Ohgai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85DE-3523634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product- beta-urogastrone
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319..477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= beta-lactamase
308..318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*rag- a
/product= fusion_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..307
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    beta-lactamase fusion gene from p002701

                                                                                                                                                                                                                                                                                                                                                               Horinaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 salivary gland; ulcers; wounds, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                               Hiramatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        665
80
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                                                                                                                                                                                                                                                                                                                                                               Koumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 533;
                                                                                                                                                                                                                derivs., plasmid(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                               Nishimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 38
AAN60631
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protects beta-urogastrone and beta-lactamase collects in the periplasm of E.coli. It is therefore easy to collect and purify the product. Beta-urogastrone is the hormone of the salivary glands which supresses stomach acid secretion and promotes cell growth, so is useful for treating ulcers and wounds. Previously the product was obtd. only
                                                                             and
                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                               misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN60631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN60631 standard; DNA; 654 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 539 BP; 130 A; 116 C; 137 G; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also AAN60628, and 30-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating ulcers and wounds. Pre in small amts. from human urine.
easily recovered from the fusion protein expressed by transformants
          gene and insertion into plasmids.
                    modified by restriction sites
                                                      Disclosure; Page 56-59;
                                                                                                            P-PSDB;
                                                                                                                                             Matsushiro
                                                                                                                                                        Aoki S,
                                                                                                                                                                              (EART-) EARTH CHEMICAL COL
                                                                                                                                                                                                   02-JUL-1984;
                                                                                                                                                                                                                       02-JUL-1985;
                                                                                                                                                                                                                                             09-JAN-1986
                                                                                                                                                                                                                                                                  DE3523634-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-urogastrone - beta-lactamase fusion gene from pUG2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
hes 15; Conser
                                                                         gene for expression of beta-urogastrone transformed cells coniq. it.
                                sequence includes the sequence of claim 1 (bases 430-588)
                                                                                                                      1986-015031/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATCTGGATCCGTF 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATCTGGATCCGTT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rogastrone gene; hormone;
protein; beta-lactamase;
                                                                                                            AAP60627
                                                                                                                                                       Ohgai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                  84JP-0137691
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                                                                                                                                                                                                                                                                                                              430.
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                                                                                                                                                                                                                                                                                                                                               /product= beta-lactamase 420..429
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                        /product= beta-urogastrone
                                                                                                                                                                                                                                                                                                                        /label= adaptor
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                                                                                                                                                                                                                                                                                                                                                                                       /product=
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                                                                                                                                                                                                                                                                                                                                                                                ..419
                                                                                                                                                       Horinaka
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100.0%;
                                                                                                                                                                                                                                                                                                              . 588
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                                                     92pp; German.
                                                                                                                                                                                                                                                                                                                                                                                          fusion_protein
                                                                                                                                                       A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15;
Pred. No.
                    for coupling to the beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      salivary gland; ulcers; wounds;
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                        Hiramatsu
           Beta-urogastrone can then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
ett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.
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                                                                                       its derivs.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                       Koumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                        Ś
                                                                                                                                                        Nishimura
                                                                                       plasmid(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 39
AA193990
ID AA193
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Best Local s
Matches 15
                                                                                                                             Ouery Match
Best Local
                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The fusion protein is less easily degraded by proteases and so protects beta-urogastrone and beta-lactamase collects in the periplasm of E.coli. It is therefore casy to collect and purify the product. Beta-urogastrone is the hormone of the salivary glands which supresses stomach acid secretion and promotes cell growth, so is useful for treating ulcers and wounds. Previously the product was obtd. only in small ants. from human urine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids originating in gene expressed in human neurobiastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, mallynamcy and susceptibility indicator or tumour marker for the contract of the
                                                                                                                                                                                                            Sequence 847
                                                                                                                                                                                                                                                               to that for N-myc and TrkA genes.
                                                                                                                                                                                                                                                                                      gene information for diagnosing prognosis is related to factors similar
                                                                                                                                                                                                                                                                                                             The invention relates to novel genes (AA.93956-AA.167963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 83; 2979pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakagawara A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIB-) CHIBA PREFECTURE.
(HISM.) HISAMITSU PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2000; 2000JP-0159195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2001; 2001WO-JP01629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43-8HP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human neuroblastoma expressed polynucleotide SEQ ID NO 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI93990 standard; cDNA: 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 654 BP;
212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598 AGATCTGGATCCGTT 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 AGATOTOGATOGGTT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-cancer agents
GAGATOTGGATOCGT 226
                                                   GAGATCTGGATCCGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-565584/63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroblastoma;
                                                                                                                             Similarity
                                                                                                         Conservative
                                                                                                                                                                                                         BP; 216 A; 238 C; 184 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                             22.7%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malignancy; cancer; tumour marker; N-myc;
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                                                                                                                             Score 15;
Pred. No.
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Pred. No.
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                                                                                                         Mismatches
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                                                                                                                                                                                                         186 T;
                                                                                                                             DB 22;
. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7;
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                                                                                                                                                                                                            23 other;
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                                                                                                                                                      Length 847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                         Indels
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                                                                                                   Gaps
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Query Match
Best Local Similarity
Watches 15; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 40
AAI94316
II)
                                                                                                                                                                                                    RESULT 41
AAZ54037/c
                                                                                                                                                                                                                                                      문
                                                                                                                                                                                                                                                                            Ŷ
                                                                                                                                                                                                                                                                                                                                                                                 wucieic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, maliquancy and susceptibility indicator or tumour marker for anti-cancer agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel genes (AA193926-AA197963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy as susceptibility indicators or tumour markers for anti-cancer agents. The
                                                                      Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection;
                                                                                                                                      21 - MAR - 2000
                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 330; 2979pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIB-) CHIBA PREFECTURE.
(HISM.) HISAMITSU PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200166719-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI94316 standard; cDNA; 883 BP
            W09957280-A2
                                    Neisseria meningitidis
                                                              antibacterial;
                                                                                                             Neisseria meningitidis ORF 629 partial DNA sequence SEQ (D NO:2023)
                                                                                                                                                                AAZ54037;
                                                                                                                                                                                       AAZ54037 standard; DNA; 969
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                 to that for N-myc and TrkA genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakayawara A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07 MAR - 2000; 2000JP - 0159195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2001; 2001WQ-JP01629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA194316
                                                                                                                                                                                                                                                      189 GAGATCTGGATCCGT
                                                                                                                                                                                                                                                                             2 GAGATCTGGATCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-565584/63.
                                                                                                                                                                                                                                                                                                                                                                                            information for diagnosing prognosis is related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroblastoma
                                                                                                                                                                                                                                                                                                                                                       883 BP; 235 A; 232 C; 187 G; 178 T; 51 other;
                                                                                                                                                                                                                                                                                                    Conscruative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                      (first entry)
                                                           qene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                   22.7%; Score 15; DB 22; 100.0%; Pied. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malignancy; cancer; tumour marker, N-myc; TrkA;
                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                         85
                                                              SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                          infection; meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO
                                                                                       antigen;
                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                Length 883;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391.
                                                                                                                                                                                                                                                                                                                                                                                              factors
                                                                          septicaemia;
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                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                              similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Overy Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-SEP-1998:
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54576 ro AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1998;
31-JUL-1998;
                                            15-FEB-2001
                                                                                                                      WO200111033-A2
                                                                                                                                                                                                Haemophilus
                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae; essential bacterial gene:
                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04 - JUN - 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF94369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF94369 standard; DNA; 1104 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 1005; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peterson J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 GTTCGACAAAACGGT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCGACAAAACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-062150/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisserial polypeptides predicted to be useful antigens % \left( 1\right) =\left( 1\right) +\left( 1\right) +\left(
                                                                                                                                                                                                                                                                                                  media; meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   969 BP; 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galeotti C, Granus ...
Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                     antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pizza M,
Venter Jo
                                                                                                                                                                                           influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                        influenzae essential bacterial gene SEQ ID N○:49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9805-0099062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0098994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.7%: Score 15; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 236 C; 317 G; 280 F; 0 other;
                                                                                                                                                                                                                                                                 upper respiratory tract ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Scalato E, :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 969;
                                                                                                                                                                                                                                                                                                          intection;
                                                                                                                                                                                                                                                                                                                                               identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   causes otitis media, meningitis and upper respiratory tract infections) which may be used as targets for potential antimicrobial agents. AAF94410 to AAF94416 represent PCR primers used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae, which encode the proteins given in AAB88492 to AAB88556. The present invention also describes methods for identifying essential bacterial genes (i.e. those essential to the survival of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2;
                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                             \tt GHPO protein; Helicobacter infection; gastroduodenal disease; qastritis; peptic ulcer disease; ss.
                                                                                                                                                                                                                                                                                                                  H. pylori GHPO 1564 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chovan LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-2000: 2000WO-US21176
          Al-Garawi A,
                                  (INMR) HUMAN GENOME SCI INC.

(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS
                                                                                     29-JUL-1997;
01-APR-1997;
                                                                                                                           01-APR-1998;
                                                                                                                                                    08-OCT-1998
                                                                                                                                                                             W09843478-A1
                                                                                                                                                                                                                                                     Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                             31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                       AAX14265;
                                                                                                                                                                                                                                                                                                                                                                                               AAX14265 standard; DNA; 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1104 BP; 347 A; 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacterium) using a transposition system. The methods are used to identify essential genes from bacteria, especially H. influenzae (which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF94345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Essential bacterial genes from Haemophilus influenzae and methods for identifying 'essential' genes that may be potential therapeutic targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB88516
                                                                                                                                                                                                                                                                                                                                                                                                                                                              729 AAAAAGCGGTAGATT 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 AAAAAGCGGTAGATT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
mes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-147511/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to AAF94409 represent essential bacterial genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hessier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                            (first entry)
          Kleanthous H,
                                                                          97US-0881227
                                                                                     97US-0902615
97US-0833457
                                                                                                                          98WO-US06371
                                                                                                                                                                                                                Location/Qualifiers
97..1122
                                                                                                                                                                                                     /*taq∸ a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.7%; Score 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reich
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                                                                                                                                                                                                                                                                                                                                                                                               ВP
          Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; 219 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 92;
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RESULT 44
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Best Local s
Matches 15
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                                                                                                                                                                                                                                                antiallergie; antidiabetie; antiuleer; anticonvulsant; antifungal; autiparasitie; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-542293/46
P-PSDH; AAW98546.
                                                                                                                                                                    17 -JAN-2001;
                                                                                                                                                                                                        Wo200159063-A2
                                                                                                                                                                                                                                        neurological disease; infection; nephrotropic; gene therapy; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                  ABA19747 standard; DNA; 1457 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1170 BP; 380 A; 180 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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APR-2000;
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08-INFC-2000

08-DEC-2000

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                                         colitis;
(d) wound
                                                                                  The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative disease, multiple sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                                                                                             The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification
                                                                                                                                                                                                                                                                                                                                                                                                        cancers and metastases
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17-NOV-2000;
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epilepsy; and and parasitic
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                                         itis; (c) cardiovascular disorders such as myocardial ischaemias; wound healing; (e) neurological diseases e.g. cerebral anoxia and
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(f) infectious infections.
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175 ACAAAACGGTAAAAA 20 ACAAAACGGTAAAAA 34 Query Match
Best Local Similarity
Matches 15; Conserv

Conservative

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Mismatches

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100.0%;

22.7%; Score 15;

Score 15; DB Pred. No. 90;

23; Length 1550

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RESULT 45
ABL02975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                   insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-AHL30511), expressed DNA sequences (AHL0184-AHL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                            capable of detecting 1000 or more genes from Drosophila. The invenuesful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1457 BP; 383 A; 345 C; 263 G; 466 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Sequence 1550
                           at ftp.wipo.int/pub/published_pct_sequences
                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                               Claim 1; SEQ ID NO 3407; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                          New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                        (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAK-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster expressed polynucleotide SEO ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL02975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL02975 standard; cDNA; 1550 BP
                                                                                                                                                                                                                               interactions
                                                                                                                                                                                                                                                                                      P-PSDB; ABB58872.
                                                                                                                                                                                                                                                                                                                                 Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
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Search completed: November 5, 2002, 08:24:50 Job time: 123.815 sees

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result.	Score	Ouery Match	Ouery Match Length	. DH	91	Description
6 -	17	25.8	456	9	AI755421	A1755421 EtESTea22
ر 2	17	25.8	559	10	BE775681	
الد	17	25.8	568	0.1	BJ008710	
4	17	25.8	630	10	BJ003054	
0 J	17	25.8		10	BJ022467	
а 6	17	25.8		12	AQ870164	
7	17	25.8		10	вк 306166	
œ	16	24.2		ç	BE213126	BE213126 lpBrn0156
0 9	16	24.2	305	12	TA104G02Q	
າ 10	16	24.2	427	12	TA104E02Q	
າ 11	16	24.2	4 3 2	<u>၂</u>	BM145840	
c 12	16	24.2	440	<u>سر</u> 22	вн170870	
o 13	16	24.2	441	9	AW462196	AW462196 BP230008B
· 14	16	24.2	442	9	AW225607	AW225607 T210058c
15	16	24.2	466	12	AQ500181	AQ500181 V15F8 mTr
16	16	24.2	478	ع	AA696283	AA696283 GM05449.5
17	16	24.2	479	10	BG520697	

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45	44	43	42	41	40	39	38	37	36	نب ای	34	ئين ئين	32 2	31	30	29	28	27	26	25	24	23	22	21	20	19	18
16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
		24.2		24.2						24.2				24.2				24.2		24.2	24.2	24.2		24.2		24.2	24.2
694	690	681	679	673	672	668	660	660	653	649	647	635	629	617	611	600	590	580	574	571	563	540	532	516	486	485	479
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B1954699	BB432863	B1582214	A2569442	BI621542	AZ572058	BI234820	AZ573452	AW690071	B1229347	AA202447	BI624045	AQ950782	BE442560	BI237091	B1568118	B1630819	A1485800	B1565318	TA55H11Q	B1612678	TA313B04P	AI457082	BI584222	BI607662	B98126	BI582395	BE444883
BI954699 HVSMEm001	BB4 32863 BB4 32863	HI582214 RH20171.5	AZ569442 26UPVH02	BI621542 RH52894.5	AZ572058 302PvH03	B1234820 RE30591.5	AZ573452 317PVE10	AW690071 NE028A06S	B1229347 RE27113.5	AA202447 LD02644.5	HI624045 RH56430.5	AQ950782 Sheared D	BE442560 WHE1103_D	BI237091 RE33250.5	HI568118 RH39495.5	BI630819 RH60131.5	AI485800 EST244121	н1565318 кн63067.5	AL456183 T. brucci	Œ.	AL490286 T. brucei	AI457082 LD37353.5	BI584222 RH23234.5	B1607662 RH74766.5	B98126 F24A16TFB I	BI582395 RH20445.5	BE444883 WHE1129_F

ALIGNMENTS

RESULT 1 AJ755421/c COMMENT REFERENCE FEATURES SOURCE KEYWORDS VERSION ACCESSION DEFINITION FOCUS AUTHORS ORGANISM JOURNAL source EtESTea22e05.yl Eimeria 5', mRNA sequence. AI755421 Email: est@watson.wustl.edu Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seq.primer: -40RP from Gibco WashU-Merck Elmeria tenella project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Liberator, P., Diaz, C., Tang, K., Marra, M., Hiller, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theisind, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Glbbons, M., Pape, D., Harvey, N., Schurk, B., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, V., Schurk, B., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, V., Schurk, B., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, V., Schurk, B., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, V., Schurk, B., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, V., Shin, T., Shin, T., Jackson, V., Shin, T., Shin, T. Eimeria tenella. Eimeria tenella Tel: 314 286 1800 Fax: 314 286 1810 Contact: David Sibley, Ph.D. Unpublished (1999) ,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and Sibley,D WashU-Merck Elmeria teneila project Eimeria AI755421.1 GI:5149068 1 (bases 1 to 456) Eukaryota: Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae; quality sequence stop: 418. /dev_stage="Sporozoite" /lab_host="SOLR E. coli" /note="Vector: Bluescript SK-; Site_1: EcoR1; Site_2: XhoI /strain="LS18" /db_xref."taxon:5802" /clone_lib="Elimeria S5-2 Sporozoite stage" Location/Qualifiers /organism-"Eimeria tenella" 456 bp mRNA linear EST 18-JAN-2000 S5-2 Sporozoite stage Elmeria tenella cDNA

; Sporozoites were obtained from in vitro sporulated and

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 17; Conservative
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Best Local Similarity
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225 GAGAFCTGGATCCGTTC 209
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                                         2 GAGATCTGGATCCGTTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial assessment of gene diversity for the comycete pathogen Phylophthora infestans based on expressed sequences Fundal Genet, Biol. 28 (2), 94-106 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Francine.Goversemedew.tyto.wau.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fel: 31 317 483 138
Fax: 31 317 483 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wageningen University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Govers F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20056376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L (bases 1 to 559)
Kamoun, S., Hraber, P.T., Sobral, B.W.S., Nuss, D. and Govers, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phytophthora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytophthora infestans
Enkaryota: stramenopiles: Oomycotes; Pythlales; Pythlaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         potato late blight agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.
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BE775681.1 G1:10229336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MY-05-E-11 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106
                                                                                   Conservative
                                                                                                                                                                                         cultured for 4 weeks in synthetic medium. EST clones were named by their position in the microtiter plate, preceded by the prefix MY (for mycellal) and the successive number of the microtiter plate (e.g. MY-06-A-04)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                excysted corysts of E. tenella grown in chickens. cDNA was synthesized from poly mRNA using an oligo-dT primer containing a Xhol site. Following second strand synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clones were converted to phagemids by mass excision Exassist helper phage and SOLR cells (Stratagene). Insert sizes range from 1.2-2.9 kb."

1.22 c 114 g 114 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EcoRI adapters were ligated to the cDNA and products were
size-selected on Sephacryl 5500. CDNAs were digested with
EcoRI/Xhol and cloned into lambda Zap II (Stratagene).
                                                                                                                                                                                                                                                                                                                         /lab_host-"E. coli, strain DH5-alpha"
/note-"Vector: psPORT1; Site_1: Sali; Site_2: Not1; Total
                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="4-week old vegetative, non-sporulating
mycelium in synthetic medium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                       kNA was isolated from mycelium of P. infestans DDR7602
                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="PinfestansMY"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref·"taxon:4787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain "DDR7602, Al mating type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism "Phytophthora infestans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to 559)
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80
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39;
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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BJ008710
                                                                                                                             Contact: Tadasu Shin-i
                                                                                                                                                  Unpublished (2001)
                                                                                                                                                                    Medaka EST Project in Takeda's lab
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Fax: 81-559-81-6855
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                                    Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                           National Institute of Genetics
                                                                                                             Center For Genetic Resource Information
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                                                                      1111 Yata, Mishima, Shizuoka 411-8540, Japan
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                tshini@genes.nig.ac.jp
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/tissue_type-"whole onbryo"
/dev_stage="segmentation stage 20
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Location/Qualifiers
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/strain="Hd-rk"
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Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
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clone bbeb0036H20r, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: tshinidgenes.niq.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-559-81-6855
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/strain."Hd-rR"
/db_xref."taxon:8090"
/clone="MF0ISSAI23DII"
/clone_lib="MF0ISSA cDNA"
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/tissue_type-"whole embryo"
/dev_stage="segmentation stage 20 -
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Oryza sativa
                                                                BF306166 927 bp mRNA linear 65F Z1-www-z 601894015F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138922 5',
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High quality sequence stop: 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Nipponbare variety using EcoRI is the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1931). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza Sativa.
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/tissue_type-"Leaf"
/tissue_type-"Leaf"
/lab_host="E. coli DH]OH"
/note-"Yector: pHACIndigo; Site_1: EcoRI; Site_2: EcoRI;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MCC http://mqc.nel.nib.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                           Ictalurus punctatus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopieryqii; Neopteryqii; Teleostei; Ostariophysi; Siluritormes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: ggapbs-r@mail.nih.gov
                                                                                                                                                                         Contact: Liu, Z.J.
                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                            Transcriptome analysis of channel catfish: I, genes and expression profiles from the brain
                                                                                                                                                                                                                                                                            and Liu, Z
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Seq primer: Mlt Reverse
                        Email: zliu#acesag.auburn.edu
                                                                                                203 Swingle Hall, Department of Fisheries, Auburn, AL 36849, USA
                                                                                                                         Amburn University
                                                                                                                                                   Fish Molecular Genetics and Biotechnology
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l (bases l to 211)
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//issne_type-"rhabdomyosarcoma"
//isb_lost_"bH10H (phaqe=reSistant)"
/note "Grqan: muscle; Vector: pUTBT; Site_1: EcoRt;
Site_2: Xhol; cDNA made by oliqo-dT priming.
blueerionally cloned into EcoR(Xhol sites using the
lorerionally cloned into EcoR(Xhol sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size L.Hkb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Herkeley) using ZAP-CDNA synthosis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 221 c 271 g 195 t I others
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/db_xre1="taxon:9606"
/elone="IMAGE:4138922"
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                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                             insert libraries for whole genome shotqun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and H. Harrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma brucei (TREU927/4 GUTat.10.1) was mechanically sheared to give a tight size distribution ( to give a tight size distribution ( 4 kb). The y+1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hall.N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., i
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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                                                                                                                                                                                                                                                                                                                                                                                       petails of T. brucei sequencing at the Sanger Centre
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a closed population of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL462316.1 GI:11831561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T. brucei sheared genomic DNA clone 104q02, reverse sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                               Email: nelsayed@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nhl⊍sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridge CB10 1SA, E-mail: barrellesanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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/strain-"TREU927"
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/db_xrof-"taxon:7998"
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                                                                                                                                                                           24.2%; Score 16; DH 12; Length 305; 100.0%; Pred. No. 1.5e+02;
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TA104E02Q

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 ACAAAACGGTAAAAAA 35
                                                                    Unpublished (2001)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                               EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and H. Barrell, Oxford University Press, 1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM145840 432 bp mRNA linear EST 30-NOV TCAAP1D8023 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project-TCAA Homo sapiens cDNA clone TCAAP8023, mF
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Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Rockville, MD. Genomic DNA isolated from a cloned population of
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                                                                                                                                                                                                           Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. an
Pediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                           Mammalia; Futheria; Primates; Catarrhini; Hominidae; l (bases 1 to 432)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Details of \Gamma. bruce: sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/\Gamma_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cambridge CB10 ISA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                      Tel: 832-824-4536
                                                                                                                                                                                                                                                                       Wei,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM145840.1
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                               Fax: 832-825-4038
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone="104e02"
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/strain="TREU927"
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                                                                                                                                                          The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                         Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                      Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Heller,C., Kim,C.J., Jeske,A., Koesema,E., Mcyers,M.C., Park,H., Prednis,L., Shinn,P., Stevenson,D.K., Zimmerman,J. and Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta:
Spermatophyta: Magnollophyta; endicotyledons; core endicots:
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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SALK_003469 Arabidopsis thallana TUNA insertion lines Arabidopsis
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                                                   Class: TDNA tagged
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                                                                                                                                ecker#salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schneider C, Hayashizaki Y, High efficiency setection of full-length cDNA by improved biotinylated cap trapper... DNA Res 4: 1, 61-6, Feb 28, 1997)"

a 74 c 88 q 173 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through nor round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P. Westover A. Nishiyama Y. Ohsumi f. 1toh M. Nagaoka S. Sasakin, Okazaki Y. Muramatsu M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGGACTGAGGGGGGGAGGAGGAGT)VN 3': V-A.C.G: N-A.C.G.J] and then do tailed. Second strand was primed with a BamHI-dC primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="TCAAP8023"
/clone_lib="Pediatric acute myelogenous leukemia cell (FAB
M1) Baylor-HGSC project=TCAA"
/sex="male"
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/dev_stage="pediatric 6 years"
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                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant Ag 99 3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi q:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
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                                                                                                                                                                                                                                                                                                        High quality sequence stop: 441.
                                                                                                                                                                                                                                                                                                                                   Seq_primer: AGCGGATAACAATTTCACACAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rovine ESTS
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Mammalia; Eutheria; Cetartiodaetyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross_match from Washington University Genome Center PHRAP suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: h lewinguiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 Mdward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
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/note-"PCR was performed on Arabidopsis_thaliana lines
each of which contains one or more TDNA insertion
clements. The resultant tragment for each line was
                    /lub_host "BH108"
/hote "Organ: placenta; Vector: pT7T3Pac; Site_1: EcoR1;
Site_2: Not1; The cDNA library was contributed by the
                                                                                                                                                             /organism-"Bos tabrus"
/db_xref-"taxon:9913"
/clone-"BP230008H10G12"
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/strain-"Columbia 0"
/db_xref-"taxon:3702"
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                                                                                                             /sex-"temale"
                                                                                                                                        /clone_lib="Soares normalized bovine placenta"
                                                                                                                                                                                                                                                                             Location/Qualitiers
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laboratory and it was constructed and normalized
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; Pred. No. 1.4e+02;
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Best Local Similarity
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395 GAGATCTGGATCCGTT 380
                                                                                                       Local Similarity
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                                       2 GAGATCTGGATCCGTT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: kate*mail.bio.tamu.edu
other name: 38 KVV-2J4; date: 12/1/99; Submitted to the Database of
Expressed Sequence Tags (dbEST) on 12/10/99; More information is
available at 'http://chrysie.famu.edu/medicago'.
Seq primer: SKmod (CTA gAA CTA gTg qAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Texas AAM University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW225607 442 bp mRNA linear EST 05
T210058e KVO Medicago truncatula cDNA clone pKV0-2J4, mRNA
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a 77 c 94 q 139 t
                                                                                                                                                                                         Inote-"Vector: pBlueScript SK -; Site_1: EcoRH: Site_2: XNIOI; cDNA was prepared from polyA: enriched RNA. The cDNA was directionally liquided into the Unizap XK vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda Zap phage using Ex-assist helper phage and propagated in XLOLE cells."
                                                                                                                                                                                                                                                                                                                                                                      /tissue_type-"Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinochizoblum mediately prior to inoculation with
/lab_host-"E.coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Medicago truncatula"
/cultivar-"qenotype A17"
/db_xref--"jaxon:3880"
/clone-"pKV0-2J4"
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100.0%; Pred. No. 1.4e+0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                  Drosophila melanogaster
Eukaryota; Melazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                       AA696283 478 bp mRNA linear EST 23-APR-20 GM05449.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM05449 5prime, mRNA sequence.
                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: anuj.kumar@yale.edu
te ot mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ross Mardonald,P., Roemer,T., Coelho,P.S.R., Agarwal,S., Kumar,A., desEtaqes,S.A., Cheund,K., H., Sheelan,A., Symoniatis,D., Jansen,R., Umansky,L., Heidtman,M., Nelson,K., Iwasaki,H., Kanada,D., Lugo,R., Hager,K., Miller,P., Roeder,G.S. and Snyder,M. Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae
Eukaryota: Fungi; Ascomycota: Saccharomycotina; Saccharomycetes;
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Contact: Stapleton, M
                   BDGP/HHMT Drosophila EST Project Unpublished (2001)
                                                                                 Harvey,D., Brokstein,P., Hong,L.,
                                                                                                      Muscomorpha: Ephydroidea; Drosophilidae; Drosophila
| (bases 1_to 478)
                                                                                                                                                                                                                      truit fly
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P.O. Box 208103, New Haven, CT 06520-8103, USA
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                                                              Lewis, S. and Rubin, G.M.
                                                                                                                                                   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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a 118 c 69 g 101 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Saccharomyces cerevisiae"
/db_xret-"taxon:4932"
/clone_lib="mTn-3xHA/lac2 Insertion Library"
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                                                                                   Evans-Holm, M., Su, C., Isang, G
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16: Conserv
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                                                                                                                                                                                             The library was constructed by Dr. Doug Jasmor (djasmer@vetmed.wsu.edu) at Washington State University, Dept. of Veterinary Microbiology and Pathology DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Rowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Isagareishvili, R., Konko, J., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and William P., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCarter, J., Clifton, S, Dante, M., Marra, M.,
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                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trichinella spiralis
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Plate: 54 row: E column: ]
                                                                                                                                                                                Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                     The Washington Univ. Nematode EST Project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: McCarter JP
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Trichinellidae; Trichinella.
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Carter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
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/clone_lib-"Trichinella spiralis ML CMVsport jasmer"
/dev_stage="muscle stage larvae"
/lab_host="DH108"
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/lab_host="solm"
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                                                                             /db_xref="taxon:6334"
                                                                                                                                                    Location/Qualifiers
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/db_xref="taxon:7227"
                                                                                                   /organism="Trichinella spiralis"
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Larvae were liberated by pepsin/HCl digestion, incubated with 1% SDS, treated with RNase and DNase to eliminate host nucleic acid contamination, and purified on a Percoll gradient. The T. spiralis isolate was obtained from Dickson Desponmier (Columbia University). The library was

The library was constructed using mRNA isolated from total RNA with oligo-dT cellulose. Total RNA was generated from muscle larvae that were isolated from injected rats.

/mote-"Vector: pCMVsport-7.neo; Site_1: Not1; Site_2: SalI

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BE444883
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The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WHE1129_F06_K11ZS Wheat etiolated seedling root normalized cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: candersn*pw.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 479)
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                                                   /note-"Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoNI: Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     provided by Dr. Doug Jasmor (d)asmor@vetmed.wsu.edu) and colleagues at Washington State University. DNA Sequencing
nystatin and cetotaxime in covered crystallization
                            the dark at room temperature on filter paper with water,
                                                                                                                               /dev_stage="Five day old etiolated seedling"
/lub_host="E. coli bH10B"
                                                                                                                                                                                                                                                                  /oultivar="Chinese Spring"
/db_xret="taxon:4565"
/clone="WHEII29_F06_KII"
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualitiers
                                                                                                                                                                                     /tissue_type-"Root"
                                                                                                                                                                                                                                           /clone_lib="Wheat etiolated seedling root normalized cDNA
                                                                                                                                                                                                                                                                                                                                                  /organism-"Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton,M., Brokstein,P., Honq,L., Tyler,D., Berman,H., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzaletz,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunco,J., Pacleb,J., Baraqas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     One Cyclotron Rd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BDGP/HHMI RH Drosophila EST Project Unpublished (2001)
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Pterygota: Neoptora; Endopterygota; Diptora; Hrachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://www.fruittly.org/EST, est@fruittly.berkeley.edu
Plate: RH.204 row: D column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lawrence Berkeley National Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Stapleton, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510 486 6798
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Anderson lab (all other authors)."
a 114 c 126 g 120 t
                   /note-"organ: head, Vector: pFlc1; Site_1: Xhol; Site_2
BamHI: Library was kindly generated by Plero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase, Plasmid cDNA library."
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                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
/db_xref:"taxon:7227"
/clone="HH20445"
/clone_lib="RH Drosophila melanogaster normalized Head
pr]c-1"
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                                                                                                                               /lab_host-"DH5-alpha TonA"
                                                                                                                                                      /dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rounsley@tigr.org
Seg primer: M13-21
Class: BAC ends
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/clone="F24A16"
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/strain-"Columbia"
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea: Drosophilidae: Drosophila.
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                                       Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Horman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, M., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta:
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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Plate: RH.747 row: F column: 6
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/db_xref="taxon:7227"
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LD37353.5prime LD Drosophila melanoquaster embryo pOT2 Drosophila
melanoquaster cDNA clone LD37353 5prime, mkNA sequence.
A1457082
                                                                                                                                                                                                                                              hit genomic sequence AL031130
Plate: 373 row: E column: 5
High quality sequence stop: 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harvey, D., Brokstein, P., Hong, L., Lewis, S. and Rubin, G.M.
HODP/HIMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                             HDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                       one Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510-486-6798
                                                                                                                                                                                                                                                                                                                                                                                     Lawrence Berkeley National Lab
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1 (bases 1 to 540)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://www.fruitfly.org/EST, estdfruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 510 486 6798
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                                                                                                                                                                                                                                                                                                               Email: http://www.fruittly.org/EST, est@fruitfly.berkeley.edu
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a 135 c 115 g 134 t 1 others
                                      /clone_lib="lb brosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 le"
/lab_bost="XL1 Blue"
                                                                                                                                  /organism="brosophila melanogaster"
/db_xref="taxon:7227"
/elone="fb37353"
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/db_xref="taxon:7227"
/elone "RH23234"
/note "organ: embryo; Vector: pOT2; Site_1: EcoKI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into
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pFlc-1"
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Pred. No. 1.4e+02;
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RESULT 25
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H1612678 HRMA linear EST 07-SEF-2001 RRMA linear EST 07-SEF-2001 RR41626.5prime RH Drosophila melanoqaster cDNA clone RH41626 5 similar to yin: FBan0002913 GC: [integral plasma membrane protein (GD:0005H87); hydroqen/ollqopeptide symporter (GD:0005427); transporter (GD:0005427); hydroqen/ollqopeptide symporter (GD:0005427); hydroqen/ollqopept
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to give a tight size distribution (
4 kb). The v i method used for the library construction is
described in detail in Smith. N. and Venter, J.C. (Making small
insert libraries for whole genome shotun sequencing projects.
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Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project. Sanger Centre, The Wellcome Trust Genome Campus, Hi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Details of T. brucel sequencing at the Sanuer Centre are available at http://www.sanger.ac.uk/Projects/T_brucel/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Constructed at the institute for Genomic Research (TIGR),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nelsayed*tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 563)
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/strain="TREU927"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila
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nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR)
                                              Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                          Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                         Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Plate: RH.416 row: C column: 2
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One Cyclotron Rd, Berkeley, CA 94720, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: nelsayed@tigr.org Details of T. bruce: sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
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                                                                                                                                                                                                                                                                                                                                                 Lawrence Berkeley National Lab
One Cyclotron Hd, Herkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J., Champe, M., Chavez, C., Dorsett, V., Fartan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paradas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Colniker, S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton, M., Brokstein, P., Hong, L., Tyler, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
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                                                                                                                                                                                                                                                                   High quality sequence stop: 515
                                                                                                                                                                                                                                                                                             Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: RH.630 row: F column: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
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/strain="TREU927"
/db_xref="taxon:5691"
/elone="55hll"
                                                                           /close_lib-"RH Drosophila melanogaster normalized Head \mathsf{pFlc}\text{-}1"
                    /sex="male and fcmale"
/dev_stage="Adult"
                                                                                                                                                                                                                                         Location/Qualifiers
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/lab_host="DH5-alpha TonA"
                                                                                                                                /clone="RH63067"
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/db_xref="taxon:7227"
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RH60181.5prime RH Drosophila melanogaster normalized Head pflc-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum
                      61801918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.qenome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact:
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                                                                                                                                                                                                                                                                                                         respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib~"tomato_ovary, "AMU"
/tissue_type="carpel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon esculentum"
/cultivar="TA496"
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Drosophila melanoqaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Endopteryyota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila

EST

truit fly.

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B1568118

611 bp mRNA linear EST 06-SEP-2001 KH839495.5prime RH Drosophila melanogaster cormalized Head pFlc-1 Drosophila melanogaster cDNA clone RH39495.5 similar to yin: PBan0002913 GO:[integral plasma membrane protein [GO:0005887]; hydrogen/oligopeptide symporter [GO:0005427]; hydrogen/oligopeptide symporter [GO:0005427]; integral plasma membrane protein [GO:000588, mKNA sequence.
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Plate: RH.601 row: C column: 7
High quality sequence stop: 532.
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Pterygota: Neoptera: Endopterygota: Diptera: Brachycera:
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One Cyclotron Rd, Berkeley, CA 94720, USA
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a 156 c 130 g 155 t 2 others
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hamH1; Library was kindly generated by Picro Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
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/db_xret="taxon:7227"
/clone-"RH60131"
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                                                                                                                                                                                                                                                                Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Munqail, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                               One Cyclotron Rd, Berkeley, Fax: 510 486 6798
                                                                                                                                 Unpublished (2001)
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta:
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilldae; Drosophila
[] (bases ] to 617)
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B1237091.1 GI:14705552
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Plate: RH.394 row: H column: 11
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Unpublished (2001)
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Email: http://www.fruitfly.org/EST, est@truitfly.berkeley.edu
                                                                       Lawrence Berkeley National Lab
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/db_xref="taxon:7227"
/clone="RH39495"
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100.0%; Pred. No. 1.3e+02;
'''^matches 0;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       Email: Oandersnapw.usda.gov
Email: Oandersnapw.usda.gov
Sequence have been trimmed to remove vector sequence and low
sequence have been trimmed score less than 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T., Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.

The structure and function of the expressed portion of the wheat
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Triticum aestivum
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WHEI1U3_D05_H09ZS Wheat etiolated seedling root normalized CDNA
library Triticum aestivum cDNA clone WHEIIU3_D05_H09, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                     West Area, Western Regional Research Center
800 Buchaman Street, Albany, CA 94710, USA
Tel: 5105595773
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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/db_xref="taxon:7227"
/clone="RE33250"
/clone="RE33250"
/clone_lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
/tissue_type="Root"
/dev_stage="Five day old etiplated seedling"
/lab host="E. coll DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
                                                                                                                                                                         /organism-"Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha TonA"
                                                                                                                                /clone_lib-"Wheat eticlated seedling root normalized cDNA
                                                                                                                                                      /clone="WHE1103_D05_H09"
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                                                                                                                                                                                                                                                                                                                                                                                         Class: shotqun
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bmail: nelsayed#tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TLGK. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tlgr.org/tdb/mdb/tbdb/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l (bases l to 635)
El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii.C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C., and Adams,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other_GSSs: Sheared DNA-51K2.TR
Contact: Najib M. El-Sayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ950782 DNA linear 635 bp DNA linear Sheared DNA-51K2.TF Sheared DNA Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1994) padsilghdun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       betermination of clone end sequences from Trypanosoma brucei GUTat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma brucei.
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AQ950782.1
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                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13-Forward
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Yelone_lib-"Sheared_DNA"

/Moster-Typector: pUClB; SetE_l: Smal; Constructed at The Institute for Genomic Esternic (TIGR), Rockville, MD. Genomic INAA isolated from a cloned population of Trypanosoma brucel (TREU92774 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)." 14.2 \, \mathrm{cm} = 157 \, \mathrm{g} + 168 \, \mathrm{t}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pHlucscript SK; Site_1: EcoKl; Site_2: Xhof; Seeds were surface-sterilized, germinated and grown ascetteally in the dark at room temperature on filter paper with water, nystatin and cetotaxime in covered crystallization
                                                                                                                                                                                                                                           /strain "TREU927/4 GUTat 10.1"
/db_xret "taxon:5691"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen
                                                                                                                                                                                                                  /clone-"Sheared DNA-51K2"
                                                                                                                                                                                                                                                                                                          /organism:"Trypanosoma brucei"
                                                                                                                                                                                                                                                                                                                                                            Location/Qualitiers
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Pred. No. 1.3e+0;
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genomic clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RH56430.5prime RH Drosophila melanogaster normalized Head pFic-1 prosophila melanogaster cDNA clone RH56430 5 similar to ylu: FBan0002913 GO:[integral plasma membrane protein (GO:0005887); hydrogen/oliquepetide symporter (GO:0005427); hydrogen/oliquepetide symporter (GO:0005427); transporter (GO:0005215); integral plasma membrane protein (GO:0005887), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: http://www.fruitfly.org/EST, est#fruitfly.berkeley.edu
Plate: RH.564 row: C column: 6
High quality seguence stop: 551.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BDGP/HHMI RH Drosophila EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Museomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheala; Hexapoda; Insecta; Pterygota; Neoptera; Endopteryqota; Diplera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
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                                                                                  /note="Organ: head: Vector: pElel: Site_1: Xhol: Site_2: BamHI; Library was kindly generated by Piezo Carninei at the RIKEN. The library was normalized and excised using Cre recombinase, Plasmid cDNA library."
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124 c 98 g 250.**
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                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone-"RH56430"
                                                                                                                                                                                       /lab_host-"DH5-alpha TonA"
/note="Organ: head; Vector:
                                                                                                                                                                                                                                      /dev_stage-"Adult"
                                                                                                                                                                                                                                                          /sex="male and female"
                                                                                                                                                                                                                                                                                           /clone_lib-"RH Drosophila melanogaster normalized Head
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                      Length 647;
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JOURNAL
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      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                              GACAAAACGGTAAAAA 330
                                                                                                                                                                                                                                 RE27113.5prime RE Drosophila melanoqaster normalized Embryo pFlc-1
Drosophila melanoqaster cDNA clone RE27113 5 similar to yin:
FBan0002913 'transporter' located on: X 4AI-4AI;: 04/12/2001, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
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649 bp mRNA linear EST 19-APR-20
LD02644.5prime LD Drosophila melanogaster embryo BlueScript
LD02644.5prime LD Drosophila melanogaster cDNA clone LD02644 5prime, mRNA sequence
                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                      В1229347
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Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BDGP/HHMI Drosophila EST Project
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  Stapleton, M.,
                           Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 653)
                                                              Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota: Neoptera: Endopterygota; Diptera: Brachycera;
                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                   sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 26 row: D column: 8
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One Cyclotron Rd, Berkeley, CA 94720, USA
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1 (bases 1 to 649)
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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                         (bases I to
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Synthesis kit. Oligo dT-primed and directionally cloned at
ECORI and XhoI in BlueScript. SK(+/-) "
163 c 145 g 172 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="LD Drosophila melanoqaster embryo BlueScript"
/sex="male and female"
/dev_staqq="0 to 24 hours mixed stage cmbryonic"
/lab_host="SOLR"
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/db_xref="HDGP_EST:BDcln002311"
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100.0%;
Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson
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Pred. No.
                                                                                                                                                                                                                                                                                                    653 bp
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Rest Local Similarity
Thinks 16; Conserv
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                           Mcdinado truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachcophyta;
Envinadophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,J., Champe,M., Chavez,C., Dorsett,V., Farian,D., Frisc,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunco,J., Pacteb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Ceiniker,S. and Rubin,G.M.
                  Plate: 028 row: A column: 06
Seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                       Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 660)
He, X.-Z., Shadle, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NF028A06ST1F1000 Developing stem Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: RE.271 row: B column: 1
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                                                         Email: radixon@noble.org
                                                                                                                                              The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK
                                                                                                                                                                                       Plant Biology Division
                                                                                                                                                                                                                 Contact: Dixon RA
                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                      Medicago truncatula stem library
                                                                                                                                                                                                                                                                               Expressed Sequence Tags from the Samuel Roberts Noble Foundation
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                                                                                                                                                                                                                                                                                                                      ., Flores, H.R., Inman, J.T., Weller, J.W.,
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1 165 c 144 g 171 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"brosophila melanoqaster"
/db_xret="taxon:7227"
/clone="RE27113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex-"male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha TonA"
Location/Qualifiers
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RESULT 48
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660 bp DNA linear GSS 15-MAY 417PVELO PV MBN #30 Plasmodium vivax genomic 3', DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dept. of Pathobiology, College of Veterinary Medicine
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                                                                                                                                                and finally centrifuged through a 50% Percoll density cushion. Puritied DMA was digested with mung bean nuclease in the presence of 44% tormamide at 500C as described (Vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). Digested DNA was blunt coded with 74 Nam Digested DNA was blunt coded with 74 Nam Digested DNA was
                                                                                                                                                                                                                                                                                                                                                           /note-*Vector: pHluescript SK(+) vector DNA, phagemid excised from lambda ZAP; Site_1: EroR V; Site_2: EroR V; Host leukocytes were extracted from P, viva. Infected blood using the following methods: first, intected blood was activated by the addition of 0.5 ml of ADP (40mg/ml) per 10 ml blood. Then blood was passed over a column of per 10 ml blood.
ligation mixture."
165 c 90 g
                                                    SK(+), and E. coli XL-10 Gold transformed with the
                                                                             over a Sepharose CL-2B column. Fractions in the size range 500bp-4kb were ligated into the Eco RV site of pBluescript
                                                                                                                                                                                                                                                                                  filter, followed by passage through a column of pre-wet Whatman CFII powder (1:2 ratio volume of blood to CFII),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type-"stem"
/dev_stage "Pooled developmental"
                                                                                                                               blunt ended using T4 DNA Polymerase and size fractionated
                                                                                                                                                                                                                                                                                                                                       acid washed 0.1 mm glass beads, then through a Plasmodipur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="asexual blood forms"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib-"Developing stem"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_bost~"Saimiri boliviensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Salvador I (Collins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Plasmodium vivax"
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Drosophila melanogaster cDNA clone RE30591 5 similar to yin:
FBan0002913 'transporter' located on: X 4Al-4Al;: 05/12/2001, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .J., Champe.M., Chavez,C., Dorsett,V., Fartan,D., Frise,E., George,R., Gonzalez,M., Guarit,H., Harris,N., El,P., Lido,G., Misra,S., Mundall,C.J., Nunoo,J., Pacleb,J., Paragus,V., Fork,S., Phouanenavong,S., Wan,K., Yn,C., Lewis,S.E., Celniker,S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stapleton, M., Brökstein, P., Hong, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: http://www.truitfly.org/EST, est@fruitfly.berkeley.edu
Plate: RE.305 row: H column: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BDGP/HHMI RE Drosophila EST Project
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                                                                                                                                                                                       /note-"Organ: embryo; Vector: pFlcl; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                   /sex-"male and female"
/dev_stage-"0-24 hours mixed stage embryonic"
/lab_host-"DH5-alpha "ronA"
                                                                                                                                                                                                                                                                                                                                                                       PFIC-
                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RE Drosophila melanogaster normalized Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="brosophila melanogaster"
/db_xref="taxon:7227"
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                                                                                                     Score 16: DB 10: Length 668; Pred. No. 1.3e+02:
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Pred. No. 1.3e+02;
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DEFINITION SOUCH A2572058/c RESULT 40

A2572058 672 bp DNA Li 302PvH03 Pv MBN #30 Plasmodium vivax genomic

672 bp

linear

GSS 15-MAY-2001

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LOCUS
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RH52894.5prime RH Drosophila melanogaster cormalized Head pPlc-1 Drosophila melanogaster cDNA clone RH52894.5 similar to yin: PHAn0002913 GO:[integral plasma membrane protein (GO:0005887); hydroqen/ollqopeptide symporter (GO:0005427); hydroqen/ollqopeptide symporter (GO:000527); hydrogen/ollqopeptide symporter (GO:000527); h
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Carlton,J.M.-R. and Dame,J.B.
The Plasmodium vivax and P. berghoi gene sequence tag projects
Drosophila melanogaster
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Class: shotqun.
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Fax: 352 392 9704
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2015 SW 23rd Avenue, Bldg 1017, Gainesville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dept. of Pathobiology, College of Veterinary Medicine
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AZ572058.1 GI:13984956
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                                             truit tly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         over a Sepharose CL-2B column. Fractions in the size range 500bp\text{-}4kb were ligated into the Eco RV site of pBluescript SK(1), and E. coll XL-10 Gold transformed with the ligation mixture."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the presence of 44% formamide at 50oC as described (Vernick, K.D., Imberski, R.B., and McCutchan, T.P. 198 Nucleic Acids Research 16:5883-5896). Digested DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Filter, followed by passage through a column of pre-wet Whatman 5F11 powder (1:2 ratio volume of blood to CF11), and finally centrifuged through a 50% percoll density cushion. Purified DNA was digested with mung bean nuclease
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excised from lambda ZAP; Site_1: EcoR V; Site_2: EcoR V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                blunt-ended using T4 DNA Polymerase and size fractionated
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/strain="Salvador I (Collins, W. 1972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Carlton,J.M.-R. and Dame,J.B.
Carlton,J.M.-R. and Dame,J.B.
The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today 16 (10), 409 (2000)
                                                                                                                                                                                                                                                                                                                                                     Plasmodium vivax
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 674)
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                   Tel: 352 392 4700
Fax: 352 392 9704
                                                                                                                                                                                                           Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
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Plate: RH.528 row: H column: 10
High quality sequence stop: 565.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   malaria parasite P. vivax.
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                                                                                              Class: shotqun.
                                                                                                                Seq primer: M13(-20) forward
                                                                                                                                            Email: damej@mail.vetmed.ufl.edu
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/dev_stage="Adult"
/lab_host="DH5-alpha FonA"
/lab_host="DH5-alpha FonA"
/note="Organ: head: Vector: pFlc1: Site_1: Xho1: Site_2:
AmnH1: Library was kindly generated by Piero Carninci at
the RIXEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
a 168 c 152 g 179 t
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/db_xref="taxon:7227"
/clone="RH52894"
/strain-"Salvador I (Collins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RH Drosophila melanogaster normalized Head pF1c-1"
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                         /organism="Plasmodium vivax"
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AUTHORS
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                                                                                            High quality sequence stop: 510
                                                                                                                                                                                            one Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                   Lawrence Berkeley National Lab
                                                                                                                                                                                                                                                                                                                               Contact: Stapleton, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Munqail,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phonanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton, M., Brokstein, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enkaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopteryqota; Diptera; Brachyœera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B1582214.1 G1:15473636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B1228414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farian, D., Frise, E., George
                                                                                                                                   Plate: KH.201 row: F column
                                                                                                                                                               Email: http://www.truittly.org/EST, est@fruittly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                          )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases ] to 681)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Vector: pBlueScript SK(+) vector DNA, phagemid excised from lambda ZAP; Site_1: Ecok V; Site_2: Ecok V; Blost leukocytes were extracted from P. Vivax intected blood using the following methods: first, infected blood was activated by the addition of 0.5 ml of ADP (40mg/ml) per 10 ml blood. Then blood was passed over a column of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Vernick, K.B., Imberski, R.B., and McCutchan, T.E. 1988. 
Nucleic Acids Research 16:6883:6896). Digested DNA was 
blunt-ended using T4 DNA Polymerase and size fractionated 
over a Sepharose CL-28 column. Fractions in the size range 
500bp-4kb were ligated into the Eco RV site of pHluescript
                                                               Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SK(+), and E. coli XL-10 Gold transformed with the ligation mixture."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cushion. Purified DNA was digested with mung bean nuclease in the presence of 44% formamide at 50oC as described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and finally centrifuged through a 50% Percoll density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           filter, followed by passage through a column of pre-wet Whatman CFII powder (1:2 ratio volume of blood to CFII),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid washed 0.1 mm glass beads, then through a Plasmodipur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib "PV MBN #30"
/dev_stage="asexual blood forms"
/lab_host "Saimiri boliviensis"
/organism·"Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:5855"
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RUMBOS KEYWORDS VERSION Ś

ORIGIN

FEATURES

Yamanaka, L., Aizawa

COMMENT

TITLE

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                                                                                                                                                                                                                                                                                                Email: genome-resigsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp/
Carnheci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carnheci.p., Shibata,Y., Mayatsu,N., Sugahara,Y., Shibata,K., Itoh
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Oaawa,K., Tanuka,T., Matsura
asa, Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)

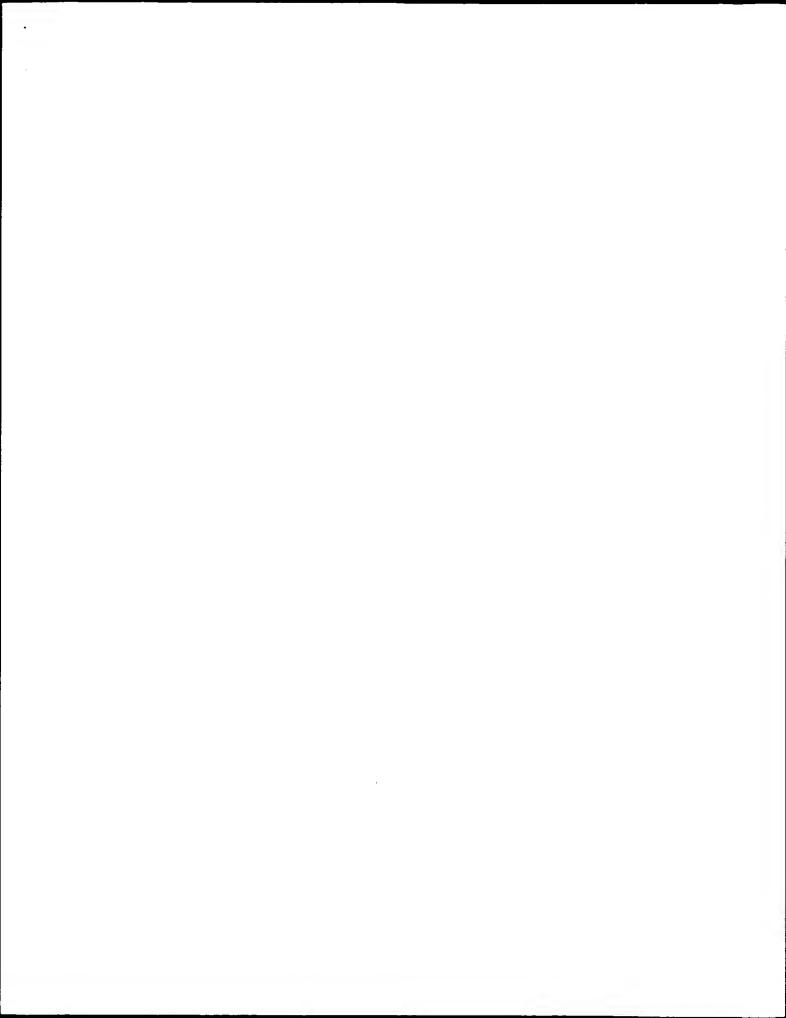
On Jul 18, 2000 this sequence version replaced q1:9272590

Contact: Yeshihide Hayashizaki
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encyclopedia: real-time sequence clustering for construction of a monredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,L., Aiza
                                                                                                                                                                                    sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757–1771 (2000)
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88432863 RIKEN full-length enriched, adult male hippocampus Mus
                                                                                                                                                                                                                                                                                   Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic
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                                                                                                                         ,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system - 484-format
                                                                                        Computer based methods for the mouse full-length cDNA
                                                                                                                                                Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Suqahara
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/clone-"RH20171"
/clone_lib="RH_Drosophila_melanogaster_normalized_Head_pElc-1"
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/lab_host "DH5-alpha TonA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                         JOURNAL
                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 GACAAAACGGTAAAAA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 GACAAAACGGTAAAAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                        Contact: Wing RA
                                                                                                                                                                                                  1 (bases 1 to 694) Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVSMEm0019F17f Hordeum vulgare green seedling ESI library HVCDNA0014 (Blumcria infected) Hordeum vulgare cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    further details.
Clemson University Genomics Institute
                                                                                                                                                      Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R. and Main,D.
                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                BI954699.1 GI:16300423
                                                                                                                                                                                                                                                                                                                                                                                                                                           BI954699
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                                                                               CDNA library
                                                                                                     for barley genomics: Blumeria infected Morex (compatible) seedling
                                                                                                                              Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                             sukaryota: Viridipiantae: Streptophyta: Embryophyta: Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HVSMEm0019F17t, mRNA sequence.
                                                                                                                                                                                                                                                         Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer adapter of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Site_1: XhoI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="hippocampus"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hippocampus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Mus musculus"
/strain-"C578L/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex∵"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="C630048D20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.28; Score 16; DB 9; I
100.08; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Search completed: November 5,
Job time: 798.981 secs
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Best Local Similarity
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                                                                                                                                                                                     45 TACCGTCCTACGAATT 60
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                                                                                                                                                                                                                                                                                                                                                                                                 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   864 656 4293
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rwing dclemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million ptu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin) Phagemids were plated and picked at the clemson University Genomics Institute (CUGI) (Requm, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, UNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            green seedlings were intected with isolate 5874 of Blumcria graminis f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-inoculation and snap frezen (Wise) In the IJ close lab at the University of California,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: pBluescript SK(): Site_1: EcoRI; Site_2 XhoI: Morex (mla) plants were greenhouse grown in the R Wise lab at lowa State University, Ames, TA; 7 day old
                                                                                                                                                                                                                                                                                                                                                                                              (http://wheat.pw.usda.gov/gqpaqes/bqn/31/cover.html)"
1 171 c 128 g 179 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genome.clemson.cdu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="green seedling leaf"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Hordcom vulgare green seedling EST library HVcDNA0014 (Blumeria intected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence analysis sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              above, For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar="Morex"
/db_xref="taxon:4513"
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                                10:51:56
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1155...59.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Query Match Length	DB	ID	Description
-	27.6	41.8	600	12	FR0003332	Z87115 F.rubripes
2	25.4	38.5	382	10	BE318413	BE318413 NF038809L
	25.4	38.5	447	9	AW690926	AW690926 NF034F11S
4	25.4	38.5	474	S	AL366452	AL366452 MtBA08A07
5	KI UI	38.5	510	9	AA660506	
6	25.4	38.5	587	9	AW693673	AW693673 NF067A03S
7	25.4	38.5	587	10	В1308971	BI308971 EST530381
œ	25.4	38.5	645	10	BF648610	BF648610 NF049E12E
9	25.4	38.5	651	9	AW696944	AW696944 NF112E09S
10	25.4	38.5	661	ی	AW685420	AW685420 NF029B07N
11	25.4	38.5	680	10	BF642214	BF642214 NF067C041
2.1	25.4	38.5	688	9	AW689706	AW689706 NF023D11S
13	25.4	38.5	777	10	BC645754	BG645754 EST507373
14	25.2	38.2	459	S	A1260450	AI260450 LP04321.5
15	25.2	38.2	521	Q	AA698485	AA698485 HL04775.5
c 16	25.2	38.2	763	12	BH274021	вн274021 сн230-108
c 17	25	37.9	877	12	CNS01ZS0	AL174681 Tetraodon

ALIGNMENTS

Query Match Best Local : Matches 3:	BASE COUNT ORIGIN	FEATURES S	COMMENT V V A	AUTHORS E TITLE D JOURNAL S	3	z
Query Match 41.8%; Score 27.6; DB 12; Length 600; Best Local Similarity 66.1%; Pred. No. 18; Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;	/organism="Takifugu rubripes" /db_xref="taxon:31033" /clone=10" cosmid 022F10" /clone="022F10bE3" 156 a 135 c 141 g 136 t 42 others	ss c	Centre Hinxton, Combridge, CB10 18B. Fmail: biohelp@hqmp.mrc.ac.uk Vector: pBluescript II KS V_type: phagemid PEKJRE: KS	LigaryG., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., ElgaryG., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Brenner,S. Direct Submission Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource	287115.1 G1:1884027 287115.1 G1:1884027 287115.1 ground survey sequence. GSS; genome survey sequence. Takifuqu rubripes. Takifuqu rubripes Takifuqu rubripes Lukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryora; Metazoa; Thordata; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontide; Takifuqu.	FRO003332 600 bp DNA linear GSS 27-FEB-1947 F.rubripes GSS sequence, clone 022F10bE3, genomic survey sequence.

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359

TOTOGATCOGOTCOACAACAGOGTGATAAAAACGGGAAATTATTNTTCAGTGAAACCCGC 417

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KEYWORDS
SOURCE
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    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                    57 GATTOTGTTCCGTTCGATAAACCGATTGTAAAACGATGTCTTATCGTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GATCTGGATCCGTTCGACAAAACGGTAAAAAAAGCGGTAGATTACCGTCCTA 54
                                                                                                                             barrol modic.
Medicago truncatula
                                                                                                                                                                          AW690926.1 G1:7565585
AW690926.1 G1:7565585
RST.
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Medicago truncatula
                                                             Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I: Fabales; Fabaceae; Papilionoldeae; Trifolieae
                                                                                                                                                                                                                                        NF034F11ST1F1000 Developing stem Medicago truncatula cDNA clone NF034F11ST 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2510 Sam Noble Parkway, Ardmore, Tel: 580 221 7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Jul 14, 2000 this sequence version replaced gi:9192190 Contact: May GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Torres-Jerez, L. Scott, A.D., Harris, A.R., Gonzales, R.A., Hell, C.J., Flores, H.K., Inman, J.T., Weller, J.W., and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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    He, x.
                                               Medicago.
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                       (bases 1 to 447)
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Samuel Roberts Noble Foundation
Samuel Noble Boundation
And Division And Andrews OK 74402,
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/tissue_type="leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/fdev_stage="Pooled developmental"
/foote-"Vector: Lambda Zap; Contains a mixture of
yound, developing, mature and senescing leaves."
1 82 e 95 q 95 t
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/db_xref="taxon:3880"
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                                                                                                                                                                                                                Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire Biologie Moleculaire des Relations Plantes-Microorganismes,
                                                                                                                                                                                                                                                                                                           Contact: Genoscope
Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I: Fabales; Fabaceae; Papillonoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: radixon@noble.org
Insert Length: 447 Std Er
Plate: 034 row: F column:
                                                                                                                                                                                                                                                                                            BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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                                                                                                                                            http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                    Mt-est#toulouse.inra.fr Website
                                                                                                                                                                                              CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
                                                                                                                                                                                                                                                                  Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: TCACACAGGAAACAGCTATGAC
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,R.A.
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/note="Vector: Lambda Sap; Contains a mixture of Internodal stem segments"
a 93 c 110 q 115 t 1 others
/clone:"MtBA08A07"
                                              /organism="Medicago truncatula"
/cultivar="Jemalong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="NF034F11ST"
/clone_lib="Developing stem"
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1. .447
                          /db_xret-"taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gilbert Biology, Stanford, CA 94305-5020, USA Tel: 650 723 3232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tags from a root-hair-enriched medicago truncatula cDNA library Plant Physiol 117 (4), 1325-1332 (1998)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fa.srl@forsythe.stanford.edu
/tissuc_type-"Root hairs & tips"
/dev_Stage-"2-3 day old seedlings"
/dev_Stage-"2-3 day old seedlings"
/note-"Organ: Root; Vector: pBK-CMV; Site_1: EcoRI;
Site_2: XhoI; cDNA was synthesized from a pooled mRNA prep
from elongating root hairs (30% w/w) and 2-3cm root tips
(70% w/w). XhoI-oliqo-dI linker-primer and EcoRI
adaptors were used cDNAs was cloned unidirectionally
into Lambda ZAP Express (Stratagene), amplified, and
mass-excised into pBK-CMV vector plasmids. More
information is available at http://bio-SRLB.stanford.edu."
a 105 c 123 g 135 t 8 others
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/dev_starqc="harvested face 3 days of N-starvation"
/dev_starqc="harvested face 3 days of N-starvation"
/note="Vector; pBluescript psK; Site_1; EcoR; Site_2:
Xhol; Plants were grown in an aeroponic chamber for 14
Xhol; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm), CDNA
was prepared from polyA+ enriched RNA. The cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mass-exclsed from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centro National de Sequencage (Genoscope, Evry, France)."
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                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Jemalong"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           directionally ligated into Uni-zapXR vector
                                                                                                                                                                                                                                                                                                                                              /clone_lib="MtRHE"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .510
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Pred. No. 1e+02;
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SOURCE

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RESULT 6
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Best Local Similarity
Matches 35; Conserv
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                                                                                                                                                                                                                                                        4 GATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTA 54
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                                                                                                                                                                                                                  GATTCTGTTCCGTTCGATAAACCGATTGTAAAACGATGTCTTA1CGTCCTA 107
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Medicago truncatula
Eukaryota: Viridiplantue: Streptophyla: Ambryophyla: Trachcophyta:
Eukaryota: Magnoliophyla: eudicotyledons; core eudicots:
                                                                                                                                                                                                                                                                                             35;
                                                                                                          EST530381 GPOD Medicago truncatula cDNA clone pGPOD-10E6 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000) On Apr 14, 2000 this sequence version replaced gi:7568333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
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587 bp mkNA linear EST 20-DEC-NF067A03ST1F1019 Developing stem Medicago truncatula cDNA clone NF067A03ST 5', mkNA sequence.
                                                       в1308971.1
                                                                        BI30897
                                                                                                                            в1308971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 067 row: A column: 03
Seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago truncatula stem library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     He, X.-Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots: Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Trifolieae;
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Medicago truncatula
               barrel medic
                                                                                      mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: radixon@noble.orq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Biology Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 587)
                                                                                                                                                                                                                                                                                                                                                                                      165 a
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                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                /note-"Vector: Lambda Zap; Contains a mixture of internodal stem segments" a 118 c 146 g 158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="stem"
/dev_stage="Pooled developmental"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Developing stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="NF067A03ST"
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                                                       CI:14983298
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68.6%;
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587
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68.6%;
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Pred. No. le
                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 GATTCTGTTCCGTTCGATAAACCGATTGTAAAACGATGTCTTATCGTCCTA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GATCTGGATCCGTTCGACAAAACGGGTAAAAAAGCGGTAGATTACGGTCCTA 54
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
                                                                                                                                      Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids [; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                          Medicago truncatula
                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                                                        NF049E12EC1F1098 Elicited cell culture Medicago truncatula cDNA
ctione NF049E12EC 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          More information is available at: www.medicago.org
Seg primer: SKmod (CTA gAA CTA gtg gAT CC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enkaryota: Viridiplantae: Streptophyta: Embryophyta: fracheophyta: Spermatophyta: Magnoliophyta; endicotyledons; core endicots; kosidae; eurosids 1; Fabales; Fabaceae; Paplilonoideae; Tritolicae;
                                                                                                                 Medicago.
                                                                                                                                                                                                                                                          barrel medic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,J. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGK sequence name: MTOAZ27TK
                                                                                 (bases 1 to 645)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michael A. Grusak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in liquid nitrogen. Pod walls were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The CDNA was directionally liquied into the Unizap XR vector from Stratagene and packaged using Gigapack III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xhof: Immature pods, ranging in age from 15 to 30 days after pollination, were collected from greenhouse-grown plants. At harvest, seeds were removed from pods and isolated pod walls were collected and immediately frozen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          days after pollination"
/note-"Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type-"immature pod walls"
/dev_stage="immature pods, ranging in age from 15 to 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="GPOD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="pGPOD-10E6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar-"A17"
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Pred. No. 1c+02;
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                                                                                                                                                                                                                                                                                                                                                                                                      T.1.1.E
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                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 GATTCTGTTCCGTTCGATAAACCGATTGTAAAACGATGTCTTATCGTCCTA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTA 54
                                                                                                                                                                                                                           Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Majonliophyta; eudicotyledons; core eudicots;

Spermatophyta; Majonliophyta; endicotyledons; core eudicots;

Tracheophyta; Majonliophyta; endicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                        Email: radixon@noble.org
Insort Length: 651 Std Er
Plate: 112 row: E column:
                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW656944 651 bp mRNA finear EST Double NF112E09STIF1070 Developing stem Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: TCACACAGAAAAGAGCTATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Biology Division
The Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Dixon RA
                                                                                                Seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                                                                                                                Fax: 580 221 7380
                                                                                                                                                                                                                                                The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
                                                                                                                                                                                                                                                                                                      Plant Biology Division
                                                                                                                                                                                                                                                                                                                                 Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula stem library
                                                                                                                                                                                                                                                                                                                                                                                                      Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                              , R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               He, X.-2., Shadle, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosidae; eurosids I; fabales; fabaceae; Papilionoideae; Tritolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       barrel medic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2510 Sam Noble Parkway, Ardmore, OK 73402, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 651)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 a
                                                                                                                                                                                                                        580 221 7302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 final concentration. Samples were taken at 0.5, 1, 24 hours after induction. Equal amounts of RNA from time point were pooled and used for mRNA isolation. If 130 c 164 q 172 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="yector: Lambda Zap; Cells were induced with yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell wall extracts equivalent to 50uq/ml glucose in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="NF049El2EC"
/clone_lib="Elicited cell culture"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula"
/db_xrof="taxon:3880"
/db_xre1="taxon:3880"
                          /organism="Medicago truncatula"
                                                                        Location/Qualifiers
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Pred. No. 1e+02;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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                                                                                                              4 GATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTA 54
                                                                      GATTOTGTTCCGTTCGATAAACCGATTGTAAAAGGATGTCTTATCGTCCTA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: nlpaiva*noble.org
Insert Longth: 661 Std Error: 0.0
Plate: 029 row: B column: 07
Seq primer: TCACACAGGAAACAGCIATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Paiva NL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watson, B.S., Shin, H.-S., Lopez-Meyer, M., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Paiva, N.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST.
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AW665420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 580 221 7317
Fax: 580 221 7380
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a mixture of young and old roots and nodules."
a 135 c 167 g 177 t
                                                                                                                                                                                                                                                                                                               /clone_lib="Nodulated root"
/lissue_type="root"
/dev_stage="Pooled developmental"
                                                                                                                                                                                                                                                                                                                                                                           /clone="NF029B07NR"
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                               /note="Vector: Lambda Zap; Four-week old Rhizobium
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68.6%;
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68.6%;
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Pred. No. 1e+02;
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Pred. No. le+02;
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RESULT 12
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Dept. of Plant Pathology
University of Arkansas
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Eukaryota; Viridiplantae: Streptophyla: Embryophyla: Tracheophyla:
Spermatophyla: Magnoliophyla: endicolyledons; core endicots;
                                                 He,X:-Z:, Shadle,G:, Scott,A.D:, Harris,A.R., Gonzale, C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D.,R.A.
                                                                                                                                                                         Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; cudicotyledons; core eudicots; Rosidae; eurosids I: Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                        NF023D11ST 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                         NF023D11ST1F1000 Developing stem Medicago truncatula cDNA clone
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Seq primer: TCACACAGGAAACAGCTATGAC:
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation
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BF642214.1 GI:11906372
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library
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                                                                                                                           1 (bases 1 to 688)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="NF067C04IN"
/clone=lib "Insect herbivory"
/clone_lib "Insect herbivory"
/clone_lib "Insect herbivory"
/tissue_type="local and systemic leaves"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants ted upon by spanded M. truncatula leaves of plants ted upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

139 c 174 g 180 t 5 others
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/db_xref="taxon:3880"
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68,6%;
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Pred. No. 1e+02;
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                                                                                                                                                                                                              M394161e TIGK sequence name: MTECG06TK More information available at: www.medicago.org Seq primer: SKmod (CTA 9AA CTA 9tg 9AT CC).
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ESTs from roots of Medicago truncatula 72 h after Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; endicotyledons; core endicots; Rosidae; enrosids 1; Fabales; Fabaceae; Papilionoideae; Tritolieae;
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BG645754
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EST507373 KV3 Medicago truncatula cDNA clone pKV3-47B11 5' end,
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Seq primer: TCACACAGGAAACAGCTATGAC
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                                                                                                                                                                                                                                                                                                         Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                                                                 College Station, TX 77843-3258, USA
                                                                                                                                                                                                                                                                                                                                                                        Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                           Department of Biology
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
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Fax: 580 221 7380
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                                                                                                                                                                                                                                                                                 Email: kate@mail.blo.tamu.edu
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/clone_llb="neveloping stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
a 139 c 176 q 189 L 3 others
/dev_stage-"3 days post-inoculation with Sinorhizobium meliloti"
                                                                                                    /organism "Medicago truncatula"
/cultivar "genotype Al7"
/db_xrej-"taxon: 880"
                                       /clone_lib="KV3"
/tissue_type="Seedling roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Medicago truncatula"
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68.6%;
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Pred. No. 1e+02;
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Best Local Similarity 68.6%;
Matches 35; Conservative
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66 TGGATCCAATGGACGAGAAGGGAAACAGGCCGGAGAATACCGCTGGACACATTC 119
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                                       TGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTACGAATTC 61
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Unpublished (2001)
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Fax: 510 486 6798
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophiltdae: Drosophila.
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A1260450
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Plate: 43 row: B column: 9
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Lewis,S. and Rubin,G.M.
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Site_2: Xho1; Sized fractionated cDNAs were directly
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/lab_host="DH5-alpha"
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/db_xref="taxon:7227"
/clone-"LP04321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                ligated into pOT2. Plasmid cDNA library.
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Pred. No. 1.2e+02;
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AA698485
LOCUS
Search completed: November 5, 2002, 08:09:53 Job time: 808.027 secs
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                                                                                     AA698485
AA6984875: Sprime HL Drosophila medanogaster bead BlueScript Drosophila medanogaster cDNA clone HL04775 Sprime similar to M59076: Mdr49 FBqn0010241 PID:q157871 SWISS-PROT:Q00449, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: http://www.fruitfly.org/EST, est@fruitfly.berkcley.edu
Plate: 47 row: G column: 3
High quality sequence stop: 378.
Location/Qualifiers
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Unpublished (2001)
Contact: Stapleton, M.
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Pteryoota: Neoptera: Endopteryoota: Diptera: Brachycera:
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BlueScript Sk; Site_1: EcoRI; Site_2: Xho!; Constructed
using Stratagene ZaP-cDNA Synthosis kit, Oligo dT-primed
and directionally cloned at EcoRI and XhoI in BlueScript
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Drosophila melanoqaster"
/db_xcct="taxon:7227"
/clone="HL04775"
/clone=lib-"HL Drosophila melanoqaster head BlueScript"
/sex="male and female"
/dev_stage="addit"
/lab_host-"SOLR"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/organism="synthetic construct" /db_xref="taxon:32630" /note="random oligonucleotide" 21 a 14 c 16 g 15 t	166	PIONEER HI-BRED INTERNATIONAL, INC. (US)	Patent: WO 0153502-A 2 26-JUL-2001;	Novel root-preferred promoter elements and methods of use	Bruce, W.B. and Niu, X.	1 (bases 1 to 66)	artificial sequence.	synthetic construct	synthetic construct.		AX203094.1 G1:15392453	AX203094	sequence 2 from Patent W00153502.	AX203094 66 bp DNA linear PAT 30-AUG-200	

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Bruce, W.B. and Niu, X.

Novel root-preferred promoter elements and Patent: WO 0153502-A I 26-JUL-2001;

PIONNER H.-BRED INTERNATIONAL, INC. (US)
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Sequence 17 from Patent W00153502
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synthetic construct
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                                                                                                                          Novel root-preferred promoter elements and methods Patent: WO 0.53502-A 18 26-JUL-2001;
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Bruce, W.B. and Niu, X.
                                                                                                            PIONEER HI-BRED INTERNATIONAL, INC.
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//db_xref="taxon:32630"
/note="synthetic sequences flanking a random oligonucleotide"
a 12 c 21 g 14 t
          /organism-"synthetic construct"
/ab_xref="taxon:32630"
/note-"synthetic sequences flanking
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48; Conserv
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Bruce, W.B. and Niu, X.
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Patent: Wo 0153502-A 15 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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AX203107
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/db_xref-"taxon:42640"
/note-"synthetic sequences flanking a random oligonucleotide"
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.9%;
Hest Local Similarity 71.2%;
Matches 47; Conservative
                                                                                         JOURNAL.
                                                                                                      TITLE
                                                                                                                                                                  ORGANISM
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                                                                                                                      AUTHORS
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                                                                                      artificial sequence.
1 (bases 1 to 66)
Bruce,W.B. and Niu,X.
Novel root-preferred promoter elements and Patent: WO 0153502-A 20 26-JUL-2001;
                                                                                                                                                                                                                      Sequence 20 from Patent W00153502
AXX031112
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Location/Qualifiers
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Bruce, W.B. and Niu, X.
Novel root-preferred promotor elements and
Patent: WO 0153502-A 16 26-JUL-2001:
                                                                         PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                                                 synthetic construct
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Sequence 22 from Patent W00153502
AX203114
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                  Homo sapiens clone RP11-12010, WORKING DRAFT SEQUENCE, 11 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent:
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                                                             Homo sapiens, clone RPII-12010
Unpublished
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                     HTG: HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       artificial sequence.
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                                                                                             Birren, B., Linton, L., Nusbaum, C.
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                                                (bases 1 to 160666)
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/db_xref="taxon:32630"
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                                                                                                                        ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                      GI:8247876
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                                                                                               and Lander, E
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Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Poliara, V., Raymond, C., Riley, R., Hogov, P., Rothman, D., Peterson, C., Poliara, V., Raymond, C., Riley, R., Hogov, P., Rothman, D., Peterson, C., Poliara, V., Raymond, C., Riley, R., Hogov, P., Rothman, D., Peterson, C., Poliara, V., Raymond, C., Riley, R., Hogov, P., Rothman, D., Peterson, C., Poliara, V., Raymond, C., Riley, R., Hogov, P., Rothman, D., Peterson, C., Poliara, V., Raymond, C., Riley, R., Hogov, P., Rothman, D., Peterson, C., Poliara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Peterson, C., Poliara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Peterson, C., Poliara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Peterson, C., Poliara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Peterson, C., Peterson, C., Peterson, R., Pet
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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Triqillo, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campopiano, A., Castle, A., Choepel, Y., Calangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the tinished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Phrap; version 0.960731
Consensus quality: 153117 bases at least 040
Consensus quality: 157272 bases at least 030
Consensus quality: 158589 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 163000; agarose-fp
Insert size: 159666; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; agarose-tp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: L7444
Center clone name: 12_0_10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815; 100% of reads
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2686 5841: cor
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1173 2585; cor
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                                                                                                                                                                                                                                                                                                                                                                                   31901: contig of 15046 bp in 32001: 9ap of 100 km
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5941: gap of 100 bp
16755: contig of 10814 bp
                                   107174: gap of 100 bp
132166: contig of 24992 bp in length
                                                                                                                                                        87576: gap of
                                                                                                                                                                                                                                                 67607: gap of
                                                                                                                                                                                                                                                                                     50522: gap of 100 bp
67507: contig of 16985 bp
132266: qap of
                                                                                                               7576: gap of 100 bp
107074: contig of 19498 bp in
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contig of 18421 bp
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TITLE JOURNAL COMMENT

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Source
Search completed: November -5, 2002, 06:26:38 Job time: 458 \pm 568 sees
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/note="assembly_tragment"
5942. .16755
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87577, 107074
/note-"assembly_fragment
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67608._.87476
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50523. ,67507
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32002. .50422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_end:SP6
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16856. .31901
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1174. .2585
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Location/Qualifiers
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                                                                                                                                                                 0; Mismatches 24; Indels
                                                                                                                                                                                                                                       1009 others
                                                                                                                                                                                            Length 160666;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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1: /SIDS1/qcqdata/qc
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/SIDs1/qcgdata/gcneseq/qeneseqn-emb1/NA2001A.DAT:*
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1181.091 Million cell updates/sec
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Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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	SUMMARIES	

		¥0			SUMMARIES	
Result.	Score	Query Match Length DB	Length		ID	Description
-	66	100.0	56	22	AAS08433	A plant root-prefe
ν.	66	100.0	56	22	AASU8453	A plant root-prefe
y.	48.4	73.3	66	22	AAS08434	A plant root-prefe
4	37.8	57.3	65	22	AAS08450	A plant root-prete
ر.	37.2	56.4	66	22	AAS08432	A plant root-prefe
5	37.2	56.4	56	22	AAS08452	A plant root-preie
7	36.2	54.8	66	22	AAS08448	A plant root-preie
œ	36	54.5	66	22	AAS08440	A random oligonucl
9	35.6	53.9	66	22	AAS08446	A plant root-prefe

4	4	4.	42	41	40	39	38	37	36	Ç.	34	3 3	32	3	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
22.4	22.4	22.4	22.4	22.4	23	23	23.2	23.2	23.2	23.2	23.2	23.4	23.6	23.6	23.6	23.6	23.8	24	24.2	24.2	24.2	24.2	24.4	24.4	24.4	24.4	24.4	25.2	25.2	25.2	26	26	34.6	35.6	35.6
33.9	ىن ر نى ن بى د	33.9	33.9	33.9	34.8	34.8	35.2	35.2	35.2	35.2	35.2	35.5	35.8	35.8	35.8	35.8	36.1	36.4	36.7	36.7	36.7	36.7	37.0	37.0	37.0	37.0	37.0	38.2	38.2	38.2	39.4	39.4	52.4	53.9	53.4
1861	1168		369	245			37096				64																								
20	22	23	23	21	23	24	21	21	21	23	22	21	24	23	23	23	23	22	22	23	2	19	21	22	23	23	22	23	23	22	18	22	22	22	2.2
AAX04212	AAF60852	AAS69854	AAS81849	AAA01453	ABL11514	AAS61380	AAA81489	AAF21611	AAA8147	ABI.09554	AAS08439	AAC94671	ABL32184	AAS70040	AAS79513	AAS70677	ABLU7964	AAS08437	AA1996	ABI.18042	AHL18043	AAV43879		AAH54503	AAS81874	AAS73285	AAH53570	ABL06834	ABL06835	AAS08445	AAV74611	AAH42733	AAS08	AAS08	AASUB44/
pAP-222 insert con	dom	DNA encoding novel	DNA encoding novel	Human colon cancer	Drosophila melanog	Human gene regulat	N. meningitidis pa	Neisseria meningit	N. meningitidis pa	Orosophila melanoq	A plant root-prefe	Cat flea hindgut a	Human immune syste	DNA encoding novel	DNA encoding novel	DNA encoding novel	Drosophila melanog	A plant root-prefe	Mycobacterium tube	Drosophila melanoq	Drosophila melanog	Mycobacterial meth	DNA encoding yeast	s. epidermidis gen	DNA encoding novel	DNA encoding novel	s. epidermidis ope	Drosophila melanog	Drosophila melanog	A plant root-prefe	Staphylococcus aur	Γ*	root	A plant root-prefe	root

С മെ 20

ALIGNMENTS

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RESULT 1
AAS08433
ID AAS0
 Root-preferred promoter element; RPE; abiotic stress; drought; salinity; pesticide resistance; herbicide resistance; biotic stress; disease resistance; tungal disease; bacterial disease; brata disease; insect attack; nematode attack; RPE14; random oliqonucleotide library;
                                                          misc_feature
                                                                                       misc_teature
                                                                                                                   misc_feature
                                                                                                                              Key
                                                                                                                                                Synthetic.
                                                                                                                                                                                                                              A plant root-preferred promoter element (RPE), RPE 14.
                                                                                                                                                                                                                                                26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                      AAS08433;
                                                                                                                                                                                                                                                                                         AAS08433 standard; DNA;
26-JUL-2001.
                   WO200153502-A2
                                                                                                                                                                     ROL; ss.
                                                                           /*tag-
/label=
19..48
/*tag-
                                                         /note:
49..66
                                                                                                                    Location/Qualitiers
                                                                  "Randomised sequence"
                               c
"3'_flanking_sequence"
                                                                                       a
"5'_flanking_sequence"
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AASUB453
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Best Local S
Matches 66
                                                                                                                                                          KOI.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonucleotide library (ROL). The invention converns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, thanking sequences, which hybridise to tissue-
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                                                                                                                                                                                       salinity; pesticide resistance; herbicide resistance; biotic stress; disease resistance; fundal disease; bacterial disease; viral disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific plant nuclear proteins, isolating the complexes and PCR amplitying the bound disponucleotide. The method is used for isolating tissue-specific promoters from plants, including but not limited to
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                                                                              mise feature
                                                                                                                          Synthetic
                                                                                                                                                                        insect attack; nematode attack; RPE21; random oligonucleotide library;
                                                                                                                                                                                                                        Root preferred promoter element; RPE; abiotic stress;
                                                                                                                                                                                                                                                     A plant root preferred promoter element (RPE), RPE 21.
                                                                                                                                                                                                                                                                                     26-SEP-2001
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"Randomised sequence"
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                                            _flanking_sequence"
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RESULT
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Best Local
                                                                                                                                                                                                                                                                        Root-preferred promoter element, RPE, abiotic stress; drought; salinity; pesticide resistance; herbicide resistance; biotic stress; disease resistance; runqal disease; bacterial disease; viral disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A plant root-preferred promoter element (RPE),
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                                                                                                                                                                                                                        insect attack; nematode attack; RPE19; random oligonucleotide library;
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Root-preferred promoter element; RPE; abiotic stress; drought;
                                   A plant root-preferred promoter element (RPE), RPE 33.
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                                                                                                                                                        DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                         73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Randomised sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "3'_flanking_sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "5'_flanking_sequence"
                                                                                                                                                        98
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48.4;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            66;
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                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                   RESULT 5
AAS08432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                  AAS08432 standard; DNA;
                                                                                                                                                                                                                                                                                                                                             Sequence 66 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442261/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bruce WB, Niu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W0200153502-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROL; ss.
                                                                                                                                                      62
                                                                                                                 62
                                                                                                                                                                                                                                                                   Local Similarity
Les 48; Conser
                                                                                                                                                    AGCTG
                                                                                                                 ACCTG
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19..48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
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achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biostress (disease resistance, resistance to attack by fungi, bacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            root-specific promoters or root-preferred promoter elements (RPE). The RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elements comprising the use of a mixture of random cligonucleotides, flanked by 5° and 3° flanking sequences, which hybridise to tissuespecific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonucleoride library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying an isolating tissue-preferred promoter elements -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   salinity, posticide resistance, herbicide resistance, biotic stress: disease resistance; fungal disease, bacterial disease; viral disease; insect attack; nematode attack; RPE33; random oliquonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 1; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2000; 2000US-0177473
                                                                                                                                                                                                                                                                                                                                                                          viruses, insects and nematodes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue-specific promoters from plants, including but not limited to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JAN-2001; 2001WO-US02011
2 GAGATCTGGATCCGTTCGGGGAAGGGAAGGTGAAAGCAAAAATTACCGTCCTACGAATTC 61
                                                                          2 GAGATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTACGAATTC 61
                                                                                                                                                                                                                                                                                               20 A; 12 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= c
/label= "3'_flanking_sequence|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                 57,3%;
73,8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
"5'_flanking_sequence"
                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                               20 G; 13 T; 1 other;
                                                                                                                                                 Pred. No. 2.7e
0; Mismatches
                                                                                                                                                                                                                        Score 37.8;
                                                                                                                                                                             8; DB 22;
2.7e-05;
                                                                                                                                                 Indels
                                                                                                                                                                                                                        Length
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                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                     amplifying the bound oligonucleotide. The method is used for isolating tissue-specific promoters from plants, including but not limited to root specific promoters or root-preferred promoter elements (RPE). The RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
                                                                                                                                                                                                                          temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonucleother library (80L). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, clinical promoter oligonucleotides, and 3/ flanking sequences, which hybridise to tissue-sequences is a plant random representation (solation to be compared promoted by 5/ and 3/ flanking sequences, which hybridise to tissue-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying an isolating tissue-preferred promoter elements.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Root preferred promoter element; RPE; abiotic stress; drought; salinity; pesticide resistance; herbicide resistance; block stress; disease resistance; fungal disease; betterial disease; viral disease; insect attack; nematode attack; RPE15; random oligonucleotide library;
                                                                                                                                                                       Sequence 66 BP; 19 A; 12 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                             achieve a desired phenotypic effect, e.g. abiotic stress (drought,
                                                                                                                                                                                                                                                                                                                                                              specific plant nuclear proteins, isolating the complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Σ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bruce WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 JAN-2000; 2000US-0177474.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roll; SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A plant root-preferred promoter element (RPE), RPE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 - SEP - 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PION ) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 - JUL - 2001
                                                                                                                     Local
6.
                                 1 TGAGATCTGGATCCGTTCGGGGAAGGGAAGGTGAAAGCAAGAATTACCGTCCTACGAATT
                                                                   I TGAGATCTGGATCCGTTCGACAAAACGGTAAAAAAAGCGGTAGATTACCGTCCTACGAATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JAN-2001;
CACCIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-442261/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Fig 1; 45pp; English
                                                                                                                     Similarity
                                                                                                                                                                                                           insects and nematodes).
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001Wo-US02011
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49.,66
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19..48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*t aq -
                                                                                                                     56.4%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Randomised sequence"
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                                                                                                                                      Score 37.2;
                                                                                                                     Pred. No.
                                                                                                      Mismatches
                                                                                                                     4.6e:05;
                                                                                                                                    DB 22;
                                                                                                      18;
                                                                                                                                    Length
                                                                                                    Indels
                                                                                                                                        66;
                                                                                                                                                                                                                                                                                                                                                              and PCR
                                                                                                    Caps
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RESULT 6
AASO8452
ID AASO
root-specific promoters or root-preferred promoter elements (RPE). The RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic
                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonucleotide library (ROL). The invention concerns a method of identifying and isolating dissour-preferred promoter elements comprising the use of a mixture of random oligonucleotides, flanked by 5' and 3' flanking sequences, which hybridise to tissuespecific plant nuclear proteins, isolating the complexes and PCB amplifying the bound oligonucleotide. The method is used for isolating tissue-specific promoters from plants, including but not limited to tissue-specific promoters from plants, including but not limited to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     salinity; pesticide resistance; herbicide resistance; biotic stress; disease resistance; fungal disease; bacterial disease; viral disease; insect attack; nematode attack; RPEF3; random oligonucleotide library;
                                                                                                                           stress (disease resistance, resistance to attack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression of nucleotide sequences in a plant comprises identifying isolating tissue-preferred promoter elements -  \frac{1}{2} \left( \frac{1}{2} \right) = \frac{1}{2} \left( \frac{1}{2} \right) \left( \frac{1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A plant root-preferred promoter element (RPE), RPE 73
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 1; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing tissue-preferred promoter elements constructs for regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WP1; 2001-442261/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-2000; 2000US-0177473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JAN-2001; 2001WO-US02011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 - JUL - 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-2001
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66 BP; 19 A; 12 C; 22 G; 14 T; 0 other;
                                                                                         insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Niu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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49..66
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/label-
19..48
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                                                                                         and nematodes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Randomised sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "5'_flanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "3'_flanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΗP
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                                                                                                                                                                                  and biotic
                                                                                                                                                                                                                                                                                                                                                                         The
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Matches

48;

Conservative

0

72.78; 56.4%;

Pred. No. 4.6e-05 Score 37.2; Mismatches

Indels Length 66;

0, Gaps

0;

DH 22; 18;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROL;
achieve a desired phenotypic effect, e.g. abiotic stress (drought temperature, salinity, pesticide and herbicide resistance) and biostress (disease resistance, resistance to attack by fungi, bacter)
                                                                                                         The sequence represents a plant root-preferred promoter element, RPE isolated from a random oligonucleotide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred prome elements comprising the use of a mixture of random oligonucleotides, flanked by 5' and 3' flanking sequences, which hybridise to tissuespectic plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating applications are sequenced.
                                                                                                                                                                                                                                                               Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Root-preferred promoter element; RPE; abiotic stress; drought; salinity; pesticide resistance; herbicide resistance; biotic stress; disease; resistance; fungal disease; bacterial disease; viral disease;
                                             RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
                                                                            rissue-specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE).
                                                                                                                                                                                                                                    Example 1: Fig 1; 45pp; English
                                                                                                                                                                                                                                                                                                                                WP I
                                                                                                                                                                                                                                                                                                                                                              Bruce WB,
                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-2000; 2000US-0177473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JAN-2001; 2001WO-US02011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_teature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 - SEP - 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS08448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS08448 standard; DNA; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insect attack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAGATCTGGATCCGTTCGACAAAACGGTAAAAAAGGGGTAGATTACCGTCCTACGAATT
                                                                                                                                                                                                                                                                                                                                2001-442261/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAGATCTGGATCCGTTCGGAGAAGGGAAGGTGAAGGCAGGAAATACCGTCCTACGAATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                root-preterred promoter
                                                                                                                                                                                                                                                                                                                                                            Nin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nematode attack; RPE89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49..66
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
19..48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- "3'_flanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Randomised sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "5'_flanking_sequence'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              element (RPE),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   random oligonucleotide library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                and biotic
                                                                                                            isolating
                                                                                                                                                                      promoter
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RESULT 8
AAS08440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
        concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonuclectides, flanked by 5° and 3° tlanking sequences, which hybridise to tissuespecific plant nuclear proteins, isolating the complexes and PCK
                                                                                                                                   Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying an isolating tissue-preferred promoter elements -
                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A random oligonucleotide library, ROL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66 BP; 19 A; 11 C; 21 G; 14 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                            W0200153502-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS08440 standard; DNA; 66 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viruses,
                                                                                                          Example 1; Page 21; 45pp; English
                                                                                                                                                                                                                       Bruce WB,
                                                                                                                                                                                                                                                (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                           21-JAN-2000; 2000US-0177473
                                                                                                                                                                                                                                                                                                      19-JAN-2001; 2001WO-US02011
                                                                                                                                                                                                                                                                                                                                 26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROL; n19813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              salinity; pesticide resistance; herbicide resistance; biotiq stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Root-preferred promoter element; RPE: abiotic stress: drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS08440;
                                                                 used to isolate tissue-specific promoter elements. The invention
                                                                             The sequence represents a random oligonucleotide library (ROL) construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insect attack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CAGCTG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CAGCTG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TGAGATCTGGATCCGTTCGACAAAACGGTAAAAAGCGGTAGATTACCGTCCTACGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGAGATCTGGATCNGTTCGGGGAAGGGAAGGTGAAAGCAAGAATFACCGTCCTACGAATT 60
                                                                                                                                                                                          2001-442261/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insects and nematodes).
                                                                                                                                                                                                                       Niu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nematode
                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
49..66
                                                                                                                                                                                                                                                                                                                                                                                                                                            /label-
19..48
/*taq=
                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                                                                                     /*taq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungal disease; bacterial disease; viral disease;
tode attack; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.8%;
71.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                "Randomised sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "5'_flanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0:
                                                                                                                                                                                                                                                                                                                                                                                      _flanking_sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.2: DB 22
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence n19813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
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amplifying the bound oligonucleotide.

The method is

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESHIT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue-specific promoters from plants, including but not limited to root specific promoters or root preferred promoter elements (RPE). The RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
                                                                               Producing tissue preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying an isolating tissue preferred promoter elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    salinity; pesticide resistance; herbicide resistance; biotic stress; disease resistance; fungal disease; bacterial disease; viral disease; insect attack; nematode attack; RPE18; random oligonucleotide library
                                                                                                                                                                                                           Bruce WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MO200123205-V5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A plant root-preferred promoter element (RPE), RPE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS08446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66 BP; 7 A; 9 C; 9 G; 11 T; 30 other;
                                                                                                                                                                                                                                                                                                                           (PION:) PIONEER HI BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                    21 JAN:2000; 2000US:0177473
                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 - JUL - 2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roof-preferred promoter element; RPE; abiotic stress; drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS08446 standard; DNA; 66 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROL; SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CAGCTC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CAGCTG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                           2001-442261/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insects and nematodes).
                                                                                                                                                                                                                                                                     Nin X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US02011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mote
49..66
/*tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*t.aq.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19..48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.5%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Randomised sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "4'_flanking_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "5'_flanking_sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 22;
Pred. No. 0.00014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Example 1: Fig 1: 45pp: English

WPI: 2001-442261/47

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS08447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonucleotide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, flanked by 5 and 3' flanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the nomplexes and PCR amplifying the bound oligonucleotide. The method is used for isolating tissue-specific promoters from plants, including but not limited to root-specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE). The RPES are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. abiotic stress (disease resistance, registance to attack by fungi, bacteria, reference in the sequence of the controlled to achieve the second stress of the controlled to achieve a controlled to achieve a serious stress (disease resistance, registance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Root-preferred promoter element; RPE; abiotic stress; drought; stalinity; pesticide resistance; biotic stress; distance; consistance; fingal discose; bacterial discose; viril discose; insect attack; nematode attack; RPE32; random oligonucleotide library
                                                                                                                                                                                                                                                                                       mise_teature
                                                                                                                                                                                                                                                                                                                                          misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A plant root-preferred promoter element (RPE), RPE 32
                                 Bruce WB, Niu X;
                                                                                                      21-JAN-2000; 2000US-0177473
                                                                                                                                                                            26 - JUL - 2001
                                                                                                                                                                                                               WO200153502-A2
                                                                                                                                                                                                                                                                                                                                                                                              misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROL; SS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 66 BP; 20 A; 12 C; 21 G; 13 T; 0 other;
                                                                (PION-) PIONEER HI-BRED INT INC
                                                                                                                                         19-JAN-2001; 2001WO-US02011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 71.2%; thes 47; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CAGCTG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FGAGATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTACGAATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insects and nematodes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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19..48
/*tag=
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/label=
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                                                                                                                                                                                                                                                                                                       "Randomised sequence"
                                                                                                                                                                                                                                                                                                                                               "5'_flanking_sequence"
                                                                                                                                                                                                                                                  "3'_flanking_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score #5.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 11
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Bost Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonucleotide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, tlanked by 5' and 3' tlanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amplifying the bound oligonucleotide. The method is used for isolatitissue-specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE).
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                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                              saliuity; posticide resistance; herbicide resistance; biotic stress disease resistance; fungal disease; bacterial disease; viral disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic
              19-JAN-2001; 2001WO-US02011
                                              26-JUL-2001.
                                                                                WO200153502-A2
                                                                                                                                              misc_feature
                                                                                                                                                                                              misc_teature
                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                ROL;
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                                                                                                                                                                                                                                                                                                                                                                                                                             A plant root-preferred promoter element (RPE), RPE 22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 66 BP; 19 A; 11 C; 21 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 1; 45pp; English
                                                                                                                                                                                                                                                                                                                                            insect attack;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGATCTGGATTCGTTCGGGGAAGGGAAGGTGAAAGCAAGAATTACCGTCCTACGAATT 60
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47: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insects and nematodes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                            ance: fungal disease: bacterial disease: viral disease:
    nematode attack: RPE22; random oligonucleotide library.
                                                                                                                                                                                         /-Lag- d
/label= "5'_flanking_sequence"
19..48
                                                                                                                                            /note= "Randomised sequence"
49..66
                                                                                                                            /*tag-
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71.2%;
                                                                                                          "3'_flanking_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.6;
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RESULT 12
AASO8451
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Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                    salinity; pesticide resistance, herbicide resistance, biotic stress; discase, resistance; fungal discase, bacterial discase, viral discase; insect attack; nematode attack; kPE71; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elements comprising the use of a mixture of random oligonuclectides, flanked by 5' and 3' flanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonucleotide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and
                                                                                                                                                                                                                                                                                                                        A plant root-preferred promoter element (RPE), RPE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 66 BP; 19 A; 11 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue-specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE). The RPEs are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
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                             misc_teature
                                                                                 misc_feature
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                                                                                                                                                    Key
                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                               AAS08451;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAS08451 standard; DNA; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amplifying the bound oligonucleotide. The method is used for isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 1; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolating tissue-preferred promoter elements
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                                                                                                                                                                                                                                                                                        Root-preferred promoter element; RPE; abiotic stress; drought
                                                                                                                                                                                                                                                                                                                                                           26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insects and nematodes).
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                                                                                                                                                                                                                                                                                                                                                        (first entry)
                             /note=
49..66
                                                                               /label=
19..48
                                                                                                                 Location/Qualifiers
1..18
/*tag- a
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71.28;
                                                "Randomised sequence"
                                                                                                _flanking_sequence'
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Pred. No. 0.00019;
0; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DH 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66;
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ANH42733
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ANH427
AC ANH42
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Hest Local Similarity
Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roof specific promoters or root preferred promoter elements (RPE). The RPES are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled to
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                                                                                                                                                                                                                                                                  A promoter element or transcription binding site
                                                                                                                                                                                                                                                                                                                 01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          achieve a desired phenotypic effect, e.g. abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance) and biotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific plant nuclear proteins, isolating the complexes and PCR amplifying the bound oligonucleotide. The method is used for isolating
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    19-JAN-2001;
                                              26 - JUL 2001
                                                                                           WO200153476-
                                                                                                                                                                                                  synthetic multimeric promoter element region; gene expression
                                                                                                                                                                                                                       Promoter element; transcription binding site; plant promoter; SMPER;
                                                                                                                                                                                                                                                                                                                                                        AAH42733;
                                                                                                                                                                                                                                                                                                                                                                                                   AAH42733 standard; DNA; 26 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stress (disease resistance, resistance to attack by fungi, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue-specific promoters from plants, including but not limited to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PION-) PIONEER HI-BRED INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 JAN-2000; 20000S-0177473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 JUL 2001
                                                                                                                                                                           insect resistance; herbicide resistance; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolating tissue-preferred promoter elements -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 ACCTIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GAGATCTGGATCGGTTCGGGGAAGGGAAGGTGAAAGTAAGAATTACCGTCCTACGAATCC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GAGATCTGGATCCGTTCGACAAAAGGGTAAAAAAGCGGTAGATTACCGTCCTACGAATTC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-442261/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insects and nematodes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Niu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
    2001WO | US02024
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US02011.
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    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.6; DB 22;
Pred. No. 0.00048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   indels
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AAV74611
ID AAV74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
  05-JAN-1996;
                                            07-JAN-1997;
                                                                                                                                                                                                                                                                                       misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                      misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxic shock syndrome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV74611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-476118/51
                                                                                                                                 EP786519-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-1999
                                                                                      30-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Niu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aureus
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regions (SMPERs). The specification describes plant promoters which comprise SMPERs. The plant promoters are useful in plant molecular biology, particularly in regulating gone expression to plants. The promoters are especially useful for transforming plants or plant ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression in plants to increase resistance against insects or herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New plant promoters with synthetic multimeric promoter element regions, useful in plant molecular biology, particularly in regulating gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ecllulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer readable medium; vaccine; S. aureus intection; immunodetection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus contig SEQ ID #300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV74611 standard; DNA; 3181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH42709-72 represent promoter elements or transcription binding sites. They are used to to construct synthetic multimeric promoter element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 BP; 12 A; 4 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 1; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2000; 2000US-0177437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AAACGGTAAAAAAGCGGTAGATTACC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAACGGTAAAAAAGCGGTAGATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       increase resistance against insects or herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
97EP-0100117
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/note= "t
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/*tag- a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "these bases represent a line of missing text in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.48;
                                                                                                                                                                                                                                 "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
                                                                                                                                                                                                                                                                                                                                                                                                 the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence.
                                                                                                                                                                                             given in the specification for this DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transforming plants or plant cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0:
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RESULT 15
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AASO84445
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           industrial importance can be obtained. Specifically, sequences which are Likely to encode antiques have been identified and these polypeptides can be used in a vaccine composition against S.aureus intection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound intections. Scaled Sin syndrome, toxic shock skin and surgical wound intections. Scaled Sin syndrome, toxic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the Slaureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the S.aureus DNA sequences allows putative functions to be assigned so that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stored on computer readable medium and
anti-S.aureus vaccines
                                                              misc_feature
                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                   insect attack;
                                                                                                                                                                                                                                                                                                                                                                                     disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                 salinity; pesticide resistance; herbicide resistance; biofic stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Root-preferred promoter element; RPE; abiotic stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A plant root-preferred promoter element (RPE), RPE 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS08445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS08445 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1194 CAGCTG 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3181 BP; 1005 A; 549 C; 483 G; 1022 T; 122 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         syndrome, etq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1: Page 1128-1130; 3271pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide(s) and proteins derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-374922/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CACCIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGAGATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTACGAATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAATATATGGACCAGTTATGTTAATTGGTTTACAAGCATTAGATTATGTACCTAAAAAAAG 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                   ance: fungal disease: bacterial disease; viral disease;
nematode attack; RPE5; random oligonucleotide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Organisms transformed with the DNA sequences can be used
                    /label= "5'_flanking_sequence"
19.47
/*tag- b
                                                                                                                                                                                       Location/Qualifiers
/note- "Randomised sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.48;
62.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dillon PJ,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kunsch CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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Search completed: November Job time: 100.942 secs

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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a plant root-preferred promoter element, RPE, isolated from a random oligonucleotide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture of random oligonucleotides, flanked by 5° and 3° flanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR specific plant nuclear proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       achieve a desired phenotypic effect, e.g. abiotic stross (drought, temperature, salinity, pesticide and herbicide resistance) and bio-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue-specific promoters from plants, including but not limited to root-specific promoters or root-preferred promoter elements (RPE). The RPES are useful in the genetic manipulation of a plant when operably linked to a nucleotide sequence whose expression is to be controlled that the controlled of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442261/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bruce WB, Niu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-2000; 2000US-0177473
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 65 BP; 18 A; 14 C; 17 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stress (disease resistance, resistance to attack by fungi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1; 45pp; English
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60 CAGCTC
                                                                     61 CAGCTG
                                                                                                                                          1 TOAGATCTGGATCCGTTCGAGCAGTAAAAGTAAGAAAGGCCCGTT-TCGTCCTACGAATI 59
                                                                                                                                                                                                            1 TGAGATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTACGAATT 60
                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insects and nematodes).
65
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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Listing first 45 summaries
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1 US -08 -484 -105 -5
2 US -09 -356 -952 -12
2 US -09 -265 -315 -32
4 US -09 -265 -315 -32
4 US -09 -265 -317 -32
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4 US -09 -091 -725 -12
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5 US -08 -444 -646 -5
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4 US-09-103-040A-1

US-08-748-947A-1

US-08-277-231A-1

US-08-473-750-4

US-08-484-105-15

US-08-484-106-15

US-08-484-106-15

US-08-233-008A-1

US-08-233-008A-1

US-08-233-008A-7

US-08-743-637B-27
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4 30.9 2156 4 US-08-965-762-18	Sequence)7 3 US-08-688-988-7	140	30.9	20.4	44	0
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43 20.4 30.9 585 4 US-08-867-902F-3 44 20.4 30.9 1407 3 US-08-688-988-7 45 20.4 30.9 2156 4 US-08-965-762-18	Sequence	72 3 US-09-249-448-33	47	30.9	20.4	4.2	
42 20.4 30.9 472 3 US-09-249-448-33 43 20.4 30.9 585 4 US-08-867-902F-3 44 20.4 30.9 1407 3 US-08-688-988-7 45 20.4 30.9 2156 4 US-08-965-762-18	Sequence	72 3 US-09-249-461-33	47	30.9	20.4	41	
41 20.4 30.9 472 3 US-09-249-461-3 42 20.4 30.9 472 3 US-09-249-448-33 43 20.4 30.9 585 4 US-08-867-902F-3 44 20.4 30.9 1407 3 US-08-688-988-7 45 20.4 30.9 2156 4 US-08-965-762-18	Sequence	12 3 US-08-809-455-33	47	30.9	20.4	40	
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36 20.4 30.9 472 2 US-08-461-965-33 36 20.4 30.9 472 2 US-08-634-641-33 37 20.4 30.9 472 3 US-09-249-71-33 38 20.4 30.9 472 3 US-09-249-472-33 39 20.4 30.9 472 3 US-09-249-452-33 40 20.4 30.9 472 3 US-08-809-455-33 41 20.4 30.9 472 3 US-09-249-461-33 42 20.4 30.9 472 3 US-09-249-461-33 42 20.4 30.9 472 3 US-08-868-988-7 43 20.4 30.9 472 3 US-08-888-988-7 44 20.4 30.9 1895 4 US-08-688-988-7 45 20.4 30.9 2156 4 US-08-688-988-7	Sequence	72 2 US-08-486-399-33	47	30.9	20.4	34	
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31 20.4 30.9 423 1 US-08-470-179-85 32 20.4 30.9 472 2 US-08-486-397-33 34 20.4 30.9 472 2 US-08-486-397-33 35 20.4 30.9 472 2 US-08-486-399-33 36 20.4 30.9 472 2 US-08-641-965-33 37 20.4 30.9 472 2 US-08-634-641-33 38 20.4 30.9 472 2 US-08-634-641-33 39 472 2 US-08-634-641-33 39 472 3 US-09-249-471-33 39 20.4 30.9 472 3 US-09-249-451-33 40 20.4 30.9 472 3 US-09-249-451-33 41 20.4 30.9 472 3 US-09-249-481-33 42 20.4 30.9 472 3 US-09-249-488-33 43 20.4 30.9 472 3 US-09-249-488-33 44 20.4 30.9 472 3 US-08-868-988-7 45 20.4 30.9 1895 4 US-08-868-988-7 46 20.4 30.9 1895 4 US-08-868-988-7 47 20.4 30.9 2156 4 US-08-965-762-18	Sequence)3 4 US-08-867-902F-2	30	30.9	20.4	30	c
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GENERAL INFORMATION:

APPLICANT: Martinis, Susan A.
APPLICANT: Sassanfar, Mandana
APPLICANT: Kim, Sundhoon
APPLICANT: Loe, Sand Ho
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL METHIONYL-THNA
TITLE OF INVENTION: SYNTHETASE GENES, TESTER STRAINS AND ASSAYS

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LOCATION:
US-08-584-226-1
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC·DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Mili
                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CPI94-05Z
                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/305,766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                        STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/584,226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                NAME/KEY: CDS
                                                                                                                                                                                                                                                                                      NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C
                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02173-4799
                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                    Brook, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Two Militia Drive
                                                                                                                                       2290 base pairs
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                                                                                      linear
                                                                     other nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bb 1125606 TFTGGACCTGCTCGGCCAGGCCCAAACCAGCGGTCGTTCGCCGCCGTAGGTGTTCGGCT 1125547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09381862
Patent No. 6245906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09103840A Patent No. 6294328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
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Best Local Similarity 62.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FRASER, Claire M.
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE.
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                  APPLICANT: Keshi, Hiroyuki
APPLICANT: Matsuhisa, Akio
TITLE OF INVENTION: PROBES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 4403765
                                                                                                                CORRESPONDENCE ADDRESS: 0'Toolo, Gerstein, Murray & Borun
COMPUTER READABLE FORM
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                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                  TITLE OF INVENTION: CAUSED BY STREPTOCOCCUS PYOGENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1488 G 1488
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                                       COUNTRY
                                                           STATE:
                                                                                                   STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6. TOTIGATECIGETEGACAAAACGGTAAAAAAGGGGTAGATTACGGTCCTACGAATTCAGCT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 FOTGGATCCGTTCGACAAAACGGTAAAAAACGGTAGATTACCGTCCTACGAATTCAGCT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Conservative
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                 60606
                                                                        Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WHITE, Owen R.
                                                         Illinois
                                                                                              233 South Wacker Drive/6300 Sears Tower
                                     United States of America
                                                                                                                                                                                                                                                             Abe, Kanako
                                                                                                                                                                                                                                                                                   Deyama, Hiroshi
                                                                                                                                                                                                    PROBES FOR THE DIAGNOSIS OF INFECTIONS
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Pred. No. 1.7;
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US-09-381-862-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EESTI. 4
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08484105 Patent No. 5589341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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APPLICANT: STILLMAN, Bruce
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                                COMPUTER READABLE FORM
                                                                                                                                                                CORRESPONDENCE ADDRESS:
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LENGIH: 3549 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 23-MAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 19
FILING DATE: 25-MAR-1997
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                                                                                                                                                                             TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES NUMBER OF SEQUENCES: 24
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                                                                                      STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.40
                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CAGC 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Cawley, Jr., Thomas A. REGISTRATION NUMBER: 40,944
 COMPUTER:
                   MEDIUM TYPE:
                                                                                                                                            ADDRESSEE:
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REFERENCE/DOCKET NUMBER: 19036/36274
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                                                        94111-4187
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                                                                                                                                                                                                                  GAVIN, Kimberly
                                                                                                                                                                                                                                                                                                       RINE, Jasper
FOSS, Margit
                                                                                                                                                                                                                                                                      LAURENSON, Patricia
                                                                                                                                                                                                                                                     HERSKOWITZ, Ira
                                                                                                                                                                                                                                                                                        McNALLY, Francis J
                                                                                                                                                                                                                                                                                                                                            KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                                                                                             BELL, Stephen P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes
IBM PC compatible
                                                                                                                                            FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
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                 Floppy disk
                                                                                                                                                                                                                                 Joachim J
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59.48;
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Pred. No. 9.6;
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: MOLECULE TYPE: US-08-484-105-5
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
(COMPUTER: IHM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AITORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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LOCAL Similarity 61.0%; Pred. No. 11;
has 36; Conservative 0; Mismatches 23; Indels 0
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TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
                                                                                          NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                 ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTACGAATTCA 62
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                                                                                                                                                                                                                                                                                                                                                                California
                                                                                                                                                                                                                                                                                                                                                                                                     TE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAURENSON, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McNALLY, Francis J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOSS, Margit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RINE, Jasper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BELL, Stephen P
                                                                                                                                                                                                                                                                                                                                                  CUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HERSKOWITZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KUBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIII.LMAN, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.30
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US-08-484-106-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 30652 GCTGAGAATGAATTCCACAAAACGATCTGAAAGATTTAGTTTGCCATCAACCGTATCCA 30594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match

33.6%, Score 22.2; DB 3;
Best Local Similarity 61.0%; Pred, No. 21;
Matches 36; Conservative 0; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/08714918 Patent No. 6037123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cole, Philip
APPLICANT: KUTIYAN, JOHN
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-228N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Margarit, S. M.
APPLICANT: Bor-Sogi, Dafna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/356,952 CURRENT FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/093,631
                                                                                                                                                                                                                        APPLICANT: Heaton, Hret
APPLICANT: Lee, Ving
APPLICANT: Malouin, François
APPLICANT: Marili, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1586 GCTGAGAATTGCACAAAACGATCTGAAGATTTAGTTTGCCATCAACCGTAIGCA 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 43676
                                                                                                                                                                            APPLICANT: Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCU
TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                         NUMBER OF SEQUENCES:
                                                     STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTACGAATTCA 62
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STRANDEDNESS: double
COUNTRY:
                     STATE:
                                              CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2700 base pairs
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                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                     California
                                                                                                                                                                                                                                              Martin, Patrick K.
Schmid, Molly B.
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                                                                                                                                                                                                    STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
                                                                                                                                                           111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.:
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90071-2066

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; Patent No. 6187541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: WARDLING, RICHARD J.

RECISTRATION NUMBER: $2,327
REFERENCE/DOCKET NUMBER: $22,005
TELESTOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPACE: (213) 955-0440
TELEX: 67-4510
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 8.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sim, Denote:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILLING DATE: December 22, 1995
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                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHI, DONGXU
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Benton, Bret
                                                                                                                                                                                                                                   ADDRESSER: Lyon & Lyon
STREET: 633 West Filth Street
STREET: 531te 4700
CITY: Los Angeles
                   APPLICATION NUMBER:
                                                                         OPERATING SYSTEM:
                                                                                                   COMPUTER:
                                                                                                                                                                                 ZIP: 90071-2066
                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                    STATE:
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                                                          SOFTWARE: Word Pertect 5.1
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Malouin, Francois
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                                                                                               IBM Compatible
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March 9, 1999
                                                                           THM P.C.
                                                                                                                                                                                                                                                                                                                                           TARGET GENES
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                   US/09/265,315
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US-09-265-315-32/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.5%;
Best Local Similarity 61.8%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DISKETTE, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Comparible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1669 ATCTGAATCCTTTTCACNAAAAGTAAAAGAAGGTAAAAGCTACCCTCGTATCATT 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                    SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THILE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                      STREET: 633 West Pifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: Septem
                                                                      FILING DATE:
                                                                                                                                                APPLICATION NUMBER: US/09/265,315 FILING DATE: March 9, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
FILING DATE:
                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPULOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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                    APPLICATION NUMBER:
                                    FILING DATE:
                                                        APPLICATION NUMBER:
                                                                                          APPLICATION NUMBER: 08/714,918
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                                                                                                                                                                                                                                                                                                                    90071-2066
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67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1810 base pairs
                                                                                                                                                                                                                                                                                                                                    U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sun, Dongxu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmid, Molly B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Henton, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                              Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: 60/009,102
December 22, 1995
September 15, 1999
                                    December 22, 1995
                                                                        September 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         September 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       = = = =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVE ON STAPHYLOCOCCUS AUREUS TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60/003,798
                    60/003,798
                                                        60/009,102
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ER: 240/247
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Pred. No.
                                                                          1996
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ATTORNEY/AGENT INFORMATION:

NAME:

Warburg, Richard J

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/U9266417 Patent No. 6228588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 33.3%;
Best Local Similarity 61.8%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1669 ATCTGAATCCTTTTCACNAAAAGTAAAAGAAGGTAAAAGCTACCCTCCTATCATT 1615
                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                          FILING DATE: September 1 AITORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ACTIVE ON STAPHYLOCUCCUS AUREUS TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sun, Dongxu
TITLE OF INVENTION: MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                               APPLICATION NUMBER: 60/009,102
FILING DATE: Decombon
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                       REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: March
                                                                                                                                                                                                                                                                                                                                                                                                                                              219:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 ATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTACGAAT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                            90071-2066
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                                                                                                           Warburg, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67-3510
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Malouin, François
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martin, Patrick K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Benton,
                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                                                  March 9, 1999
                                                                                                                                           September 15, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHODS OF SCREENING FOR COMPOUNDS
                                                                                                                                                          60/003,798
                                                                                                                                                                                                                                                                                                     US/09/266,417
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                                                                       240/248
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Pred. No.
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COCATION: 177..219; OTHER INFORMATION: US-09-091-725-18
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 Matches
                              Query Match
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                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1669 ATCTGAATCCTTTTCACNAAAGTAAAAGGTAAAAGCTACCCTCGTATCATT 1615
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                            PEATURE
                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                         HYPOTHETICAL: I
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STRANDEDNESS: single
                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 95203620.0 FILING DATE: 22-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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               Local Similarity
                                                                                                           NAME/KEY:
                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                        PAPE:
                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                 E. Victor Donahue
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 Conservative
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177.
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                                                                                                                                            Phaffia rhodozyma
                                                                                                                                                                                                                       linear
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61.8%;
               33.0%; Score 21.8; 61.4%; Pred, No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and recombinant DNA for use therein
                                                                             /product= "PRertY"
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                                                                                                                                                                                                                                                                                                                                                                                   EP 96200943.7
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                                                                                                                                                                                                                                                                                                                    35,492
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Pred. No. 12;
Mismatches
                 15;
                              DB 4; Length 2470;
 22;
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                                                                                                                                                                         RESULT 13
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                                                                                                                     Sequence 22, Application US/09091725
Patent No. 6329141
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Patent No. 6329141
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                             Mat ches
                                                                                                                                                                                                                                                                                                          Best Local Similarity 61.4%;
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                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                       2216 TOTOCTCATGACCERATGCGGAAGGGGAAGAAGAATACCGACAGACAA 2272
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NAME: E. Victor Donahue
                  CORRESPONDENCE ADDRESS:
                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MODES NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIFLE OF INVENTION:
                                 NUMBER OF SEQUENCES:
                                                                                      APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                  TEATURE:
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FILING DATE: 22-DEG
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                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /product: "PRCITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Phatfia rhodozyma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
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ADDRESSEE: Morrison & Foerster lip
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                                                                                                                                                                                                                                                          1 TGAGATCTGGATCCGTTCGACAAAACGGTAAAAAAGCGGTAGATTACCGTCCTACGA 57
                                                                                                                                                                                                                                                                                          35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20006 1888
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                                                 and recombinant DNA for use therein
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                                                                  Improved methods for transforming Phatfia
                                                                                                                                                                                                                                                                                                        33.0%; Score 21.8;
61.4%; Pred. No. 19
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us-09-091-725-22
                           Ouery Match 33.0%;
Best Local Similarity 61.4%;
Matches 35; Conservative
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                    FEATURE
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HYPOTHETICAL: NO
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NAME: E. Victor Donahue
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STRANDEDNESS: double
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CITY: Washington
                                                                                                   OTHER INFORMATION: /product- "PRGertB GB"
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1 TGAGATOTGGATOCGTTCGACAAAACGGTAAAAAAGCGGTAGATTAGCCGTCCTACGA 57
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967..1077
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                                          Score 21.8; DB 4; Length 3550; Pred. No. 16;
                           Mismatches
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                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08444646 Patent No. 5837263
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Best Local Similarity 63.5
Matches 33: Conservative
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TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: :
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOSYMS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION IMMA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                         APPLICANT: Hauke, David A. APPLICANT: Shang, Ellen S. TITLE OF INVENTION: Leptos
                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
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LENGTH: 730 base pairs
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ATTORNEY_AGENT INFORMATION:
NAME: LOWIS, James L.
REGISTRATION NUMBER: 24,732
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                                                                                                                                                                                                                                                                                                                                                                                                  530 GGTCGTGAGAAGAITGCAAAAGCTGGTGAFTACCGTCCTATTACTGACCCIG 58
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CITY: L
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STRANDEDNESS: both
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CITY: Washington
                                                                            STATE: California
COUNTRY: USA
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                                                                                                                    Los Angeles
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                                                                                                                                  5E: Robbins, Berliner & Carson 201 N. Figueroa Street, 5th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 466-0800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 21.6;
63.5%; Pred. No. 14;
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Search completed: November 5, 2002, 06:19:06 Job time: 1892.3 secs
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                                                                                                                                            Best
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                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Wong, Wean Khing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DCCURRENT APPLICATION DATA:
                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                             594 AGAAGTAAAAAAGGCGGTAGTTTCCAGTCCTGCGAA 629
                                                                                                                   Local Similarity 32.7%; Score 21.6; hes 27; Conservative ...
                                                                                           23 AAACGGTAAAAAGCGGTAGATTACCGTCCTACGAA 58
                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 5656-107
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                                                                                                                                                                                                                                                         TYPE
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                                                                                                                                                                                                                                                nucleic acid
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(213) 977-1003
                                                                                                                                                                                                                        linear
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    Mismatches

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